

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:57:50 ; Search time 362 Seconds  
(without alignments)  
9501.607 Million cell updates/sec

Title: US-10-621-855-4  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA.\*  
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2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
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6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1887	97.5	1889	3	US-09-489-407-16
3	1867	96.5	1878	3	US-09-187-906-14
4	1867	96.5	1878	3	US-09-489-407-14
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6	897.6	46.4	1699	3	US-09-489-407-20
7	854.4	44.2	1203	3	US-09-220-528-65
8	854.4	44.2	1203	3	US-09-949-016-3208
9	751.6	38.8	1271	3	US-09-187-906-18
10	751.6	38.8	1271	3	US-09-489-407-18
11	224.8	11.6	24984	3	US-09-949-016-14950
12	218.4	11.3	260	3	US-09-016-434-530
13	192.8	10.0	601	3	US-09-949-016-116675
14	169.8	8.8	238	3	US-09-016-434-537
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16	102	5.3	1392	3	US-09-487-685-2
17	102	5.3	1392	3	US-08-802-805D-2
18	102	5.3	1392	3	US-09-388-316C-2
19	102	5.3	1490	3	US-08-861-990-10
20	102	5.3	1888	3	US-09-187-906-12
21	102	5.3	1888	3	US-09-489-407-12
22	102	5.3	1995	3	US-08-957-063-15
23	102	5.3	1995	3	US-09-487-685-15
24	102	5.3	1995	3	US-08-802-805D-15

25	102	5.3	1995	3	US-09-388-316C-15
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27	102	5.3	2600	3	US-09-487-685-1
28	102	5.3	2600	3	US-08-802-805D-1
29	102	5.3	2600	3	US-09-388-316C-1
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31	88	4.5	670	3	US-09-487-685-19
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34	86	4.4	1392	3	US-08-957-063-5
35	86	4.4	1392	3	US-09-487-685-5
36	86	4.4	1392	3	US-08-802-805D-5
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43	86	4.4	3358	3	US-09-487-685-4
44	86	4.4	3358	3	US-08-802-805D-4
45	86	4.4	3358	3	US-09-388-316C-4

ALIGNMENTS

RESULT 1  
US-09-187-906-16  
; Sequence 16, Application US/09187906  
; Patent No. 6677135  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural  
; TITLE OF INVENTION: and Renal Growth  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Biogen, Inc.  
; STREET: 14 Cambridge Center  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02142  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/187,906  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: PCT/US97/07726  
; APPLICATION NUMBER: PCT/US97/07726  
; FILING DATE: 07-MAY-97  
; APPLICATION NUMBER: US 60/017,427  
; FILING DATE: 08-MAY-96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/019,300  
; FILING DATE: 07-JUN-96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/021,859  
; FILING DATE: 16-JUL-96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043,533  
; FILING DATE: 10-APR-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kaplan, Warren A.  
; REGISTRATION NUMBER: 34,199  
; REFERENCE/DOCKET NUMBER: A008 PCT CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-679-2400  
; TELEFAX: 617-679-2838  
; INFORMATION FOR SEQ ID NO: 16:

Sequence 15, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 17, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 4, Appl

SEQUENCE CHARACTERISTICS:

LENGTH: 1889 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 41..1231  
US-09-187-906-16

Query Match 97.5%; Score 1887; DB 3; Length 1889;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 109 GCGACCTCCACTGCTGATGATCCTGCTACTGTGTGCTGTGTGTGGCTGCCACTTGGAGC 168  
DB 61 GCGACCTCCACTGCTGATGATCCTGCTACTGTGTGCTGTGTGTGGCTGCCACTTGGAGC 120  
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DB 121 AGGAACTCCCTTGCACAGAGAAACAGGTTTGTGAACAGCTGTATCCCGAGGCCAGAAAGAA 180  
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DB 181 ATGCGAGGCTAATCCCGCTTGCAGAGCTGCTTACAGCAGCACTGGGCTCTCTGACCTCCAG 240  
QY 289 TTTAAGCAGGCGCGCTTGTAGAGAGTCTGCCATGCTGCAGACTGCCCTAGAGGCGAGC 348  
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QY 409 AGCTACCTGTCTGGACATTTATGAGACCGTTTACCGCTCCCGAGGAGCTTGGTACTACGA 468  
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; Sequence 16, Application US/09489407
; Patent No. 6861509
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; TITLE OF INVENTION: and Renal Growth
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/489,407
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1889 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 41..1231
; US-09-489-407-16

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	Matches 1887;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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901	GGCATACCTGGGCTCATTTGGGACTGCCATGACCCCAAACTTCATCAGAAGGTCAACAC	960
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1201	CTTTCCTTTGATTTCTGCTGAGACCTCTGTTAGCTGGGCTTCTCAGGGTCTTTTGTTC	1260
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Db 1321 AAGAAGAGCGCGCTGTACACAGCAACCCGGAACCAACCCAGGCAATTCGGCAGACATCC 1380  
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Db 1861 TTAATAAAAAAAAAAAAAAAAAAAAAA 1887

## RESULT 3

US-09-187-906-14  
; Sequence 14, Application US/09187906  
; Patent No. 6677135  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural  
; TITLE OF INVENTION: and Renal Growth  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Biogen, Inc.  
; STREET: 14 Cambridge Center  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02142  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/187,906  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/07726  
; FILING DATE: 07-MAY-97  
; APPLICATION NUMBER: US 60/017,427  
; FILING DATE: 08-MAY-96

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/019,300  
; FILING DATE: 07-JUN-96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/021,859  
; FILING DATE: 16-JUL-96  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/043,533  
; FILING DATE: 10-APR-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kaplan, Warren A.  
; REGISTRATION NUMBER: 34,199  
; REFERENCE/DOCKET NUMBER: A008 PCT CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-679-2400  
; TELEFAX: 617-679-2838  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1878 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 205..1242  
; US-09-187-906-14  
  
Query Match 96.5%; Score 1867; DB 3; Length 1878;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
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LOCUS Mus musculus glial cell line-derived neurotrophic factor family
DEFINITION receptor alpha 3 (gfra3) mRNA, complete cds.
ACCESSION AF036163
VERSION AF036163.1 GI:2674176
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Naveilhan,P., Baudet,C., Mikaelis,A., Shen,L., Westphal,H. and
AUTHORS Ernforb,P.
TITLE Expression and regulation of GFRA3, a glial cell line-derived
neurotrophic factor family receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (3), 1295-1300 (1998)
PUBMED 9448325
REFERENCE 2 (bases 1 to 1911)
AUTHORS Naveilhan,P. and Ernforb,P.
TITLE Direct Submission
JOURNAL Submitted (28-NOV-1997) Lab. Mol. Neuro. Dept. Medical Biochemistry
and Biophysics, Karolinska Institute, Doktorsringen 12A, Stockholm
171 77, Sweden
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DEFINITION	Ret ligand (RetL) for stimulating neural and renal growth.									
ACCESSION	BD195079									
VERSION	BD195079.1 GI:33004837									
KEYWORDS	JP 2002515743-A/10.									
SOURCE	unidentified									
ORGANISM	unclassified.									
REFERENCE	1 (bases 1 to 1889)									
AUTHORS	Nadel,M.S., Hession,C. and Cate,R.L.									
TITLE	Ret ligand (RetL) for stimulating neural and renal growth									
JOURNAL	Patent: JP 2002515743-A 10 28-MAY-2002;									
COMMENT	OS Unidentified PN JP 2002515743-A/10 PD 28-MAY-2002 PR 07-MAY-1997 JP 1997542431 PR 08-MAY-1996 US 60/017427, 07-JUN-1996 US 60/019300 PR 16-JUL-1996 US 60/021859 PI MICHELE SANICOLA NADEL,CATHERINE HESSION,RICHARD L CATE PC C07K14/47,C12N15/12,C12Q1/68,A61K48/00,C12N5/10,C12N15/62, PC C07K16/18, PC C12N5/06,G01N15/33 CC Strandedness: Single; CC Topology: Linear; CC Ret ligand (RetL) for stimulating neural and renal growth FH Key Location/Qualifiers FT CDS Location/Qualifiers 1..1889 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"									
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Db 1861 TTAATAAAAAAAAAAAAAAAAAAAAAA 1887

RESULT 6
LOCUS AR642126 1889 bp mRNA linear PAT 20-APR-2005
DEFINITION Sequence 16 from patent US 6861509.
ACCESSION AR642126
VERSION AR642126.1 GI:62778309
KEYWORDS SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1889)
AUTHORS Sanicola-Nadel, M., Hession, C., Cate, R.L. and Worley, D.S.
TITLE Antibodies to Ret and RetL3
JOURNAL Patent: US 6861509-A 16 01-MAR-2005;
Biogen, Inc.; Cambridge, MA
FEATURES
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ORIGIN
Query Match 97.5%; Score 1887; DB 6; Length 1889;
Best Local Similarity 100.0%; Pred. No. 0;
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## ORIGIN

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RESULT 8  
BC066202  
LOCUS

2006 bp mRNA linear ROD 08-MAR-2005

BC066202

3-MAR-2005

DEFINITION	Mus musculus glial cell line derived neurotrophic factor family receptor alpha 3, mRNA (cdna clone MGC:76710 IMAGE:6430904), complete cds.
ACCESSION	BC066202.1
VERSION	GI:42490963
KEYWORDS	MGC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 2006) Straussberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Sherman KM, Schuler GP, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RP, Jordan H, Moore T, Max SI, Wang J, Heish F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MP, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McSwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Heltan E, Kettman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skaleka U, Smalusz DE, Schnarch A, Schein JE, Jones SJ and Marra MA.
CONSTRM	Mammalian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCE	2 (bases 1 to 2006)
AUTHORS	Director MGC Project.
TITLE	Direct Submission
JOURNAL	Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000) cDNA Library Preparation: Catherine Lee, Endocrine Pancreas Consortium cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: <a href="http://www.shgc.stanford.edu">http://www.shgc.stanford.edu</a> Contact: (Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a> Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAK Plate: 144 Row: a Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31981761. Location/Qualifiers 1..2006 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="MGC:76710 IMAGE:6430904" /tissue_type="pancreas, pooled libraries Melton normalized mixed mouse pancreas 1 NI-MMS1, Amplified Melton mou se islets 1 M1S1-A, and Kaestner rgn3 wt." /clone_lib="NIH_MGC_137" /lab_host="DH10B" /note="Vector: pSPORT1" 1..2006 /gene="Gfra3" /db_xref="GeneID:14587"
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QY 1844 TGTTTAACTCTTATCTGCTCCCAATTCCTCTAGTCCCTTGGGTCAATGATTAACATT 1903  
Db 1801 TGTTTAACTCTTATCTGCTCCCAATTCCTCTAGTCCCTTGGGTCAATGATTAACATT 1860  
QY 1904 TTGACTT 1910  
Db 1861 TTGACTT 1867

## RESULT 10

BD195078  
LOCUS BD195078 1878 bp DNA linear PAT 17-JUL-2003  
DEFINITION Ret ligand (RetL) for stimulating neural and renal growth.  
ACCESSION BD195078  
VERSION BD195078.1 GI:33004836  
KEYWORDS JP 2002515743-A/9.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 1878)  
AUTHORS Nadel,M.S., Hession,C. and Cate,R.L.  
TITLE Ret ligand (RetL) for stimulating neural and renal growth  
JOURNAL Patent: JP 2002515743-A 9 28-MAY-2002;

## COMMENT

OS Unidentified  
PN JP 2002515743-A/9  
PD 28-MAY-2002  
PF 07-MAY-1997 JP 1997542431  
PR 08-MAY-1996 US 60/017427, 07-JUN-1996 US 60/019300 PR  
16-JUL-1996 US 60/021859  
PI MICHELLE SANICOLA NADEL, CATHERINE HESSION, RICHARD L. CATE PC  
C07K14/47, C12N15/12, C12Q1/68, A61K48/00, C12N5/10, C12N15/62, PC  
C07K16/18,  
PC C12N5/06, G01N15/33

CC	Strandedness: Single;	
CC	Topology: Linear;	
CC	Ret ligand (RetL) for stimulating neural and renal growth FH	
Key	Location/Qualifiers	
FT	CDS	205..1242.
FEATURES	Location/Qualifiers	
source	1..1878	
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ORIGIN		
Query Match	96.5%; Score 1867; DB 6; Length 1878;	
Best Local Similarity	99.9%; Pred. No. 0;	
Matches 1878; Conservative	0; Mismatches 0; Indels 1; Gaps 1;	
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QY	97	CTCTGGAGCCCGGACCTCCACTGCTGATGATCTGCTACTGCTGCTGCTGCTGCT 156
Db	61	CTCTGGAGCCCGGACCTCCACTGCTGATGATCTGCTACTGCTGCTGCTGCTGCT 120
QY	157	GCCACTTGGAGCAGAGAACTCCCTGCGCACAGAGAACAGGTTTGTGAACAGCTGTACCCA 216
Db	121	GCCACTTGGAGCAGAGAACTCCCTTTGCCACAGAGAACAGGTTTGTGAACAGCTGTACCCA 180
QY	217	GSCCAGAAAGAAATGCGAGGCTAATCCGCTTGCAGGCTGCTACAGGACCTCGGGCTC 276
Db	181	GSCCAGAAAGAAATGCGAGGCTAATCCGCTTGCAGGCTGCTACAGGACCTCGGGCTC 240
QY	277	CTGCACCTCCAGTTTAAAGCAGGCGCTGCCCTTTAGAGGAGTCTGCCATGTCTGCAAGACTG 336
Db	241	CTGCACCTCCAG-TTAAAGCAGGCGCTGCCCTTTAGAGGAGTCTGCCATGTCTGCAAGACTG 299
QY	337	CCTAGAGGAGCAGAGAACTCAGAGAACAGCTCTCTGATAGACTGCGAGGTGCGCATCGGCG 396
Db	300	CCTAGAGGAGCAGAGAACTCAGAGAACAGCTCTCTGATAGACTGCGAGGTGCGCATCGGCG 359
QY	397	CATGAAGCAGCAAGCTACTGCTGCGACATTTATTTGACCGTTACCTGCGCGAGGCT 456
Db	360	CATGAAGCAGCAAGCTACTGCTGCGACATTTATTTGACCGTTACCTGCGCGAGGCT 419
QY	457	TGGTGACTACGAGTTGGATGTCTCACCTTATGAAGACACAGTGACGAGCAAACTCGGAA 516
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QY	517	AATGAATCTTAGCAAGTTGAACATGCTCAACCCATGAAGACACAGTGACGAGCAAACTTTGC 576
Db	480	AATGAATCTTAGCAAGTTGAACATGCTCAACCCATGAAGACACAGTGACGAGCAAACTTTGC 539
QY	577	TATGCTGTACTCTTCAGCAAGTGTGACCGCTGCGCAAGGCTACGGGAGGCATG 636
Db	540	TATGCTGTACTCTTCAGCAAGTGTGACCGCTGCGCAAGGCTACGGGAGGCATG 599
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Db	600	CTCAGGGATCCGCTGCGAGCGCACTCTGCTCCTAGCCAGCTGCGCTCTCTTTTGAGAA 659
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Db	780	CAATTTGCTGTGATCTGCGGAGCTTCTGCGGTGCGGACCTTTTGTGAGATCAGCGCTGAT 839
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Db	840	GGACTTCCAGACCCACTGTCTATCTTATGGACATCTTTGGGACTTGTGCAACTGAGCAGTC 899
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Db	900	CAGATGTCTGCGGCGCATACCTGCGGCTGATTTGGGACTGCGCATGACCCCAAACTTTCATCAG 959
QY	997	CAAGGTCAACACTACTGTGTGCTTTAAGCTGACCTGCGGAGGAGCGGCAACCTTACAGGA 1056
Db	960	CAAGGTCAACACTACTGTGTGCTTTAAGCTGACCTGCGGAGGAGCGGCAACCTTACAGGA 1019
QY	1057	CGAGTGTGAACAGCTGGAAGGCTCTCTTCCAGAACCCCTGCTCGTGGAGGCACTTGC 1116
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QY	1117	AGCTAAGATGCTTTTCCACAGACAGCTTCTCTCCAGGACTGGGAGGCTTCTTCTTCT 1176
Db	1080	AGCTAAGATGCTTTTCCACAGACAGCTTCTCTCCAGGACTGGGAGGCTTCTTCTTCT 1139
QY	1177	AGTGGTGAGCAGCAGAGAACAGCAACCTGCTCTGAGACTGAGCCAGGCTACCCATTC 1236
Db	1140	AGTGGTGAGCAGCAGAGAACAGCAACCTGCTCTGAGACTGAGCCAGGCTACCCATTC 1199
QY	1237	TTCTTTCTCCATCTTCCCTTTGATTTCTGTCAGACCTCTGCTAGCTGGGCTTCTCTCAG 1296
Db	1200	TTCTTTCTCCATCTTCCCTTTGATTTCTGTCAGACCTCTGCTAGCTGGGCTTCTCTCAG 1259
QY	1297	GCTCTTTTGTCTCTTCCACCAACCCAGACTGATTTTGAGCTGCTGCTGGGAGAGAACTC 1356
Db	1260	GCTCTTTTGTCTCTTCCACCAACCCAGACTGATTTTGAGCTGCTGCTGGGAGAGAACTC 1319
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QY	1417	CGCAGCATCTCCCTGCTGCTCCAGAGAGGCTTTAGAGTGAAGTGAAGGCTTGTACCTCCGA 1476
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QY	1477	TCCTTAGCGGCTAGTGTTCCTTCCCTTCCCTTCTGCTTCTTCTGCTCAGGCTGCTC 1536
Db	1440	TCCTTAGCGGCTAGTGTTCCTTCCCTTCCCTTCTGCTTCTTCTGCTCAGGCTGCTC 1499
QY	1537	CTCCTTAGGACTTTGTGGGCTCAGTTTTCCTTCTGCTTCTGCTGCTGCTGCTGCTGCTC 1596
Db	1500	CTCCTTAGGACTTTGTGGGCTCAGTTTTCCTTCTGCTTCTGCTGCTGCTGCTGCTGCTC 1559
QY	1597	CTCCAGCGCTTCTTCTGCTTCCAGGACCAACCCAGAGGCTTAAGGATCAGTCACTCCCT 1656
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QY	1777	GGTGTCTGACTCTCTGCGCAGCAATCTTGAACATTTGGGCAATGAGAGCTTAAGTCTT 1836
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QY	1897	AAACATTTGACTTAAAAA 1915
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AR452067 AR452067 1878 bp mRNA linear PAT 20-FEB-2004

LOCUS Sequence 14 from patent US 6677135.

DEFINITION AR452067

ACCESSION AR452067

VERSION AR452067.1 GI:42683406

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1878)

AUTHORS Sanicola-Nadel,M., Hession,C., Cate,R.L. and Worley,D.S.

TITLE Ret ligand (RetL) for stimulating neutral and renal growth

JOURNAL Patent: US 6677135-A 14 13-JAN-2004;

Biogen, Inc.: Cambridge, MA

FEATURES

source

1..1878

Location/Qualifiers

/organism="unknown"

/mol\_type="mRNA"

ORIGIN

Query Match 96.5%; Score 1867; DB 6; Length 1878;

Best Local Similarity 99.9%; Pred.No. 0;

Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 37 CGCGCGCCCGCAGCGCAGGCGCTGTCGATCCCGGGGTCCACCGGCCATGGGCT 96

Db 1 CGCGCGCCCGCAGCGCAGGCGCTGTCGATCCCGGGGTCCACCGGCCATGGGCT 60

QY 97 CTCCTGGAGCCGCGACCTCCACTGCTGATGATCTGCTACTGCTGCTGCTGCTGCT 156

Db 61 CTCCTGGAGCCGCGACCTCCACTGCTGATGATCTGCTACTGCTGCTGCTGCTGCT 120

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Db 121 GCCACTGGAGCAGAACTCCCTTGCCACAGAGAACAGGTTGTGAACAGCTGTACCCA 180

QY 217 GSCCAGAAAGAAATCGAGGCTTAATCCGCTTGCAAGCTGCTACACAGCACTCGGGCTC 276

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Db 1860 AAACATTTTGACTTAAAA 1878

RESULT 12

AR642125

LOCUS AR642125 1878 bp mRNA linear PAT 20-APR-2005

DEFINITION Sequence 14 from patent US 6861509.

ACCESSION AR642125

VERSION AR642125.1 GI:62778308

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1878)

AUTHORS Sanicola-Nadel,M., Hession,C., Cate,R.L. and Worley,D.S.

TITLE Antibodies to Ret and RetL3

JOURNAL Patent: US 6861509-A 14 01-MAR-2005;

Biogen, Inc.; Cambridge, MA

FEATURES

Location/Qualifiers

1..1878

source

/organism="unknown"

/mol\_type="mRNA"

ORIGIN

Query Match 96.5%; Score 1867; DB 6; Length 1878;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 37 CGCGCGCCAGCGCAGGCGAGCGCTGTGCGATCCCGGGGTCCACCCGCCATGGGGCT 96

Db 1 CGCGCGCCAGCGCAGGCGAGCGCTGTGCGATCCCGGGGTCCACCCGCCATGGGGCT 60

QY 97 CTCCTGGAGCCCGGACCTCCACTGCTGATGATTCCTGTACTGTGGTGTCTGTGGCT 156

Db 61 CTCCTGGAGCCCGGACCTCCACTGCTGATGATTCCTGTACTGTGGTGTCTGTGGCT 120

QY 157 GCCACTTGGAGCAGGAATCCCTTTGCCACAGAGAACAGGTTTGTGAACAGCTGTACCCTA 216

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Db 1380 GGCAGCACTCCCTCTGCTCCAGAGAGGCTTTAGAAAGTGAAGGCTGTGACCCCTTCGGA 1439

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Db 1800 TGGGCTTGTGTTAACTCTTATTACTGTCCCAAAATCCCTAGTCCCTTTGGTTCATGATT 1859

Qy 1897 AAACATTTGACTTAAAA 1915

Db 1860 AAACATTTGACTTAAAA 1878

RESULT 13

BC079378

LOCUS

DEFINITION Rattus norvegicus glial cell line derived neurotrophic factor family receptor alpha 3, mRNA (cdna clone MGC:94884 IMAGE:7110848), complete cds.

ACCESSION BC079378

VERSION BC079378.1 GI:50927778

KEYWORDS MGC.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 2070)

AUTHORS Klausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Touchman, J.W., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalhus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

CONSRMT Mammalian Gene Collection Program Team

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

PUBMED 12477932

REFERENCE 2 (bases 1 to 2070)

AUTHORS NIH MGC Project

CONSRMT Direct Submission

TITLE Submitted (02-AUG-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA

JOURNAL NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK Contact: MGC help desk

COMMENT Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Howard Jacobs

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-ehgc.stanford.edu>

Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: TRAK plate: 182 Row: c Column: 10

This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers

source

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ORIGIN

Query Match 71.3%; Score 1379; DB 9; Length 2070;

Best Local Similarity 87.5%; Pred. No. 0;

Matches 1652; Conservative 0; Mismatches 180; Indels 55; Gaps 11;

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Db 1 GCGCGCGCGCCAGCAGCAGGCGCTGCGGCTCCGCGCTCCAGACCCGCCATGG 60

Qy 93 GGCTCTCTGAGCGCCGCGACTTCACCTGCTGATGATCCTGCTACTGTGCTGTGTGT 152

Db 61 GGCTCTCTGAGCGCCGCGACTTCGCTGCTGATGATCCTGCTACTGTGCTGTGTGT 120

Qy 153 GGCTGCCACTTGGAGCAGGAACTCCCTTGGCCACAGAGACAGGTTTCTGAACAGCTGTA 212

Db 121 GGCTACCCCTTGGAAACAGGAACTCCCTTCCACAGAGAAAGGCTTGTGAACAGCTGTA 180

Qy 213 CCCAGGCCAGAAAGAAATGCGAGGCTAATCCCGCTTGAAGGCTGCCTACCAACACCTGG 272

Db 181 CCCAGGCCAGAAAGAAATGCGAGGCTAATCCCGCTTGAAGGCTGCCTACCAACACCTGG 240

Qy 273 GCTCTGCACTCTCAGTTTAAAGAGCGCGCTGCCCTTAAAGAGAGTCTGCCATGTCTGAC 332

Db 241 ACTCTGCACTCCCGCAGTCTCAGCAGTCCACTGCCCTCAGGGGAGTCTGCCCATCTGCAG 300

Qy 333 ACTGCTAGAGGCGCAGCAGAACTCAAGTCTCTGATAGACTGTCAGGTGCCATC 392

Db 301 CGTGCTTGAAGCAGCAGCACTCAGAAACAGTCTCTCATAGACTGTCAGGTGCCAC 360

Qy 393 GCGCATGAAGCAGCAACAGTCTCTGACATTTATTTGACCGTTTCACTGCGCCGAA 452

Db 361 GCGCATGAAGCAGCAGCACTCTCTGACATTTATTTGACCGTTTCACTGCGCCGAA 420

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RESULT 15  
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LOCUS  
DEFINITION Mus musculus glial cell line-derived neurotrophic factor family  
receptor alpha-3 (gfra3) mRNA, complete cds.  
ACCESSION AF041842  
VERSION AF041842.1 GI:2921578  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS 1 (bases 1 to 1244)  
TITLE Widenfalk, J., Tomac, A., Lindqvist, E., Hoffer, B. and Olson, L.  
GFRA3, a protein related to GFRA1, is expressed in  
developing peripheral neurons and ensheathing cells  
Eur. J. Neurosci. 10 (4), 1508-1517 (1998)  
JOURNAL  
PUBMED 9749804  
REFERENCE 2 (bases 1 to 1244)  
AUTHORS Tomac, A., Hoffer, B. and Olson, L.  
TITLE Direct Submission  
JOURNAL Submitted (07-JAN-1998) Neuroscience, Karolinska Institute,  
Doktorsringen 12, Stockholm 17171, Sweden  
FEATURES  
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location/Qualifiers  
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ORIGIN

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Job time : 9939 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:57:33 ; Search time 7953 Seconds  
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11383.504 Million cell updates/sec

Title: US-10-621-855-4

Perfect score: 1935

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Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_est4:\*

5: gb\_est5:\*

6: gb\_est6:\*

7: gb\_est7:\*

8: gb\_est8:\*

9: gb\_est9:\*

10: gb\_est10:\*

11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1871.8	96.7	1919	4	AK046542 Mus muscu
2	915.6	47.3	1812	4	CR618834 full-leng
3	824	42.6	1112	11	DQ039349 Homo sapi
4	814.8	42.1	880	6	CF585129 AGENCOURT
5	745.8	38.5	958	6	CF585128 AGENCOURT
6	722.8	37.4	740	7	CK782042 UI-M-HJO-
7	633.8	32.8	667	2	BB323153 BB323153
8	603.2	31.2	973	5	BA04447 BX04447
9	598.4	30.9	600	3	BI987608 3203-65 M
10	582.4	30.1	937	5	BQ716490 AGENCOURT
11	569.8	29.4	1054	1	AL558255 AL558255
12	556.2	28.7	589	3	BP771344 BP771344
13	552.6	28.6	958	5	BX329151 BX329151
14	551.2	28.5	992	5	BX375148 BX375148
15	544.8	28.2	634	2	BB645236 BB645236
16	541.2	28.0	1060	1	AL530853 AL530853
17	516.2	26.7	815	3	BI834990 60308882
18	505	26.1	516	2	BF471500 UI-M-BH3-
19	493.6	25.5	795	7	CK483117 AGENCOURT
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23	468	24.2	932	5	BQ000978
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25	461.6	23.9	715	7	CN278586
26	452.6	23.4	499	6	CB712227
27	447.6	23.1	1138	3	BM546331
28	438.2	22.6	460	10	CG483033
29	438	22.6	853	11	DQ039350
30	434.2	22.4	856	5	BX425705
31	430.6	22.3	442	1	AA049894
32	429.8	22.2	859	5	BUI49220
33	428.6	22.1	535	6	CB718239
34	421	21.8	465	1	AA050083
35	420.8	21.7	959	5	BX370244
36	416.4	21.5	467	2	BB832607
37	413.6	21.4	473	2	BB833560
38	408.8	21.1	437	3	BI676681
39	396	20.5	445	2	BB830713
40	393.6	20.3	875	5	BQ881951
41	385.4	19.9	387	8	W99197
42	381.2	19.7	933	5	BQ718109
43	377.2	19.5	542	6	CA390626
44	369.2	19.1	405	5	BY378274
45	366.8	19.0	398	5	BY027270

#### ALIGNMENTS

RESULT 1	AK046542	AK046542	1919 bp	mrna	linear	HTC 03-APR-2004
LOCUS	Mus musculus adult male adrenal gland cDNA, RIKEN full-length					
DEFINITION	enriched library, clone:B330033018 product:glial cell line derived neurotrophic factor family receptor alpha 3, full insert sequence.					
ACCESSION	AK046542					
VERSION	AK046542.1 GI:26338184					
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1					
AUTHORS	Carninci, P. and Hayashizaki, Y.					
TITLE	High-efficiency full-length cDNA cloning					
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)					
PUBMED	10349636					
REFERENCE	2					
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.					
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes					
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)					
PUBMED	11042159					
REFERENCE	3					
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.					
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer					
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)					
PUBMED	11076861					
REFERENCE	4					
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.					
TITLE	Functional annotation of a full-length mouse cDNA collection					
JOURNAL	Nature 409, 585-590 (2001)					
PUBMED	11076861					
REFERENCE	5					
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research					

Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation  
JOURNAL of 60,770 full-length cDNAs  
REFERENCE Nature 420, 563-573 (2002)

AUTHORS 6 (bases 1 to 1919)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanaoka, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koyama, S., Kurthara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
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Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.

TITLE Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
JOURNAL Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.

## FEATURES

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## ORIGIN

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VERSION DQ039349.1 GI:66890558  
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REFERENCE 1 (bases 1 to 1112)  
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,  
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civeello, D.,  
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
A Scan for Positively Selected Genes in the Genomes of Humans and  
Chimpanzees  
(ar) PLOS Biol. 3 (6), E170 (2005)  
JOURNAL 15869325  
PUBMED 2 (bases 1 to 1112)  
REFERENCE Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,  
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civeello, D.,  
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
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VERSION	CF585128
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REFERENCE	1 (bases 1 to 958)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: <a href="mailto:cgapbe-remail.nih.gov">cgapbe-remail.nih.gov</a> Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000) cDNA Library Preparation: Catherine Lee, Endocrine Pancreas Consortium cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: IRBD10 row: g column: 09 High quality sequence stop: 683.

## FEATURES

source

RESULT 6

RESUL 6  
CK782042

CK7042  
LOCUS

## DEFINITION

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**ACCESSION**

**VERSION**

## KEYWORDS

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KEYWORDS EST.

SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## ORIGIN



10 (11), 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Yamana, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishii, Y. and Hayashizaki, Y.  
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, 172-186 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

## FEATURES

source

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/notes="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGTCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCTCGAGTAAATTAATATCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"
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## ORIGIN

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RESULT 8
LOCUS BX404447 973 bp mRNA linear EST 01-MAY-2004
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ACCESSION BX404447
VERSION BX404447.2 GI:46924437
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 973)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30635183.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3046.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CL0BB029ZH02RPI&c=3046.r.
Location/Qualifiers
1. 973
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/clone_lib="Homo sapiens NEUROBLASTOMA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector."
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## FEATURES

source



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Db 541 AGAGCGCGGTAAACACCATCGCCCCCAGTGTGGCGCCTGCTTCTGTAAACCCCAATTGCC 600

RESULT 10
LOCUS BQ716490
DEFINITION AGNCOURT_8291136_lupski_sympathetic_trunk_Homo_sapiens_cDNA_clone
IMAGE:6194172_5', mRNA sequence.
ACCESSION BQ716490
VERSION BQ716490.1 GI:21855387
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 937)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.illnl.gov
Plate: LHAM13598 row: p column: 13
High quality sequence stop: 653.
FEATURES
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/clone="IMAGE:6194172"
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/lab_host="DH10B"
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/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGTCCG-3' and
5'-GACTAGTTCTAGATCCGAGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."
ORIGIN
Query Match 30.1%; Score 582.4; DB 5; Length 937;
Best Local Similarity 84.0%; Pred. No. 1.5e-142;
Matches 669; Conservative 0; Mismatches 126; Indels 1; Gaps 1;
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QY 274 CTCCTGCACCTCCAGTTTAAAGCAGGCGCTGCTTGCAGGAGTCTGCATGCTGCGAGA 333
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Db 784 TCAGCAATGTCAACAC 799
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DEFINITION Homo sapiens cDNA clone CS0DU001YA19 5-PRIME, mRNA sequence.
ACCESSION AL558255
VERSION AL558255.3 GI:46183654
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1054)
Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31280054.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3046.r
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For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?r=CS0DU001YA100P1&c=3046.r.  
Location/Qualifiers

FEATURES

Db	864	GACCCACTGCCATCCCATATGACACTCTAGGAACCTGTGTC-AMAGAGCAGTCCAGATGTTT	922
Qy	946	GGGGGAGTACCTGGGGCTGATTGGGACTGCATGACACCCCA	985
Db	923	AC-GASMTAATCTGGGGTGTATTGGGRTKGTGACCCCAA	961
RESULT 12			
BP771344/c			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
Qy	1372	AAGAGCAGAGGTGTACACAGACACCGGACCAACAGGAGTATCCGAGACACATCCCGT	143
Db	588	AAAACGAGCGGTGCAACACAGACACCGGACCAACAGGAGTATCCGAGACACATCCCGT	529
Qy	1432	CTGCTCCAGAAAGAGGTCTTAGAAGTGAAGGCTGTGACCCCTTCCGATCTGAGCGCTAGT	149
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Qy	1492	TTTCAAAACCTCCCTTGGCCCTTCTTCTGATGGGCTCAGGCTGTCTCTTAGGACTTTG	155
Db	468	TTTCAAAACCTCCCTTGGCCCTTCTTCTGATGGGCTCAGGCTGTCTCTTAGGACTTTG	409
Qy	1552	TGGGTCCAGTTTGGCTTCTTCTGATGGGCTCAGGCTCAGCTCCAGGCTTCTTC	161
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Qy	1612	CTGTTTCCAGGACCAACCGAGGCTAAGGAATCAGTCAATTCCTGTGCTTCCAGG	167
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/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male adrenal
gland"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 185.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTCGAGTTAATTAATATCCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: Sali; 3' end:
BamHI"
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ORIGIN

Query Match	28.2%;	Score 544.8;	DB 2;	Length 634;
Best Local Similarity	96.2%;	Pred. No. 1.2e-132;		
Matches 558;	Conservative 0;	Mismatches 22;	Indels 0;	Gaps 0;
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QY	217	GGCCAGAAAGAAATCGAGGCTAATCCGCTTGCAAGGCTGCTTACAGCAGCTGGGCTC	276	
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QY	457	TGGTGACTACGAGTTGGATGTCTCACCTTATGAAGACACAGTGACCAACCCCTGGAA	516	
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 08:37:03 ; Search time 1191 Seconds  
(without alignments)  
10828.027 Million cell updates/sec

Title: US-10-621-855-4  
Perfect score: 1935  
Sequence: 1 gaattggccctcaggcca.....aaaaaaaaaaaaaaaaaaaaa 1935

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_21.\*

- 1: geneseqn1980s.\*
- 2: geneseqn1990s.\*
- 3: geneseqn2000s.\*
- 4: geneseqn2001as.\*
- 5: geneseqn2001bs.\*
- 6: geneseqn2002as.\*
- 7: geneseqn2002bs.\*
- 8: geneseqn2003as.\*
- 9: geneseqn2003bs.\*
- 10: geneseqn2003cs.\*
- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*
- 14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1935	100.0	1935	3	Aaz29100 Murine Gf
2	1887	97.5	1889	2	Aav00249 Mouse Ret
3	1887	97.5	1889	12	Adj58708 Murine re
4	1887	97.5	1889	14	Ady53844 Mouse ret
5	1887	97.5	1889	14	Adz00208 Mouse Ret
6	1867	96.5	1878	2	Aav00256 Mouse Ret
7	1867	96.5	1878	12	Adj58706 Murine re
8	1867	96.5	1878	14	Ady53842 Partial m
9	1867	96.5	1878	14	Adz00206 Mouse Ret
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11	955.2	49.4	1878	2	Aav99334 Glial cel
12	934.6	48.3	1829	3	Aaz93702 PRO538 DN
13	934.6	48.3	1829	3	Aaa88519 Human PRO
14	934.6	48.3	1829	3	Aaa77617 Human PRO
15	934.6	48.3	1829	3	Aaa54101 PRO538 cD
16	934.6	48.3	1829	13	Adt94301 Human PRO
17	934.4	48.3	1792	3	Aaz29104 Human GFR
18	933	48.2	1991	2	Aav99329 cDNA enco
19	928.2	48.0	1829	3	Aac58234 Human PRO

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22	897.6	46.4	1699	14	ADY53848	Ady53848 Human ret
23	897.6	46.4	1699	14	ADZ00212	Adz00212 Human Ret
24	854.4	44.2	1203	3	AAA12547	Aaa12547 DNA enco
25	854.4	44.2	1203	14	ADV42887	Adv42887 Human psy
26	851.4	44.0	1200	2	AAV35364	Aav35364 Human GDN
27	849.8	43.9	1200	2	AAV35365	Aav35365 Human GDN
28	821.4	42.4	1809	2	AAV99333	Aav99333 Glial cel
29	751.6	38.8	1271	2	AAV00250	Aav00250 Human Ret
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32	751.6	38.8	1271	14	ADZ00210	Adz00210 Human Ret
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34	749.8	38.7	1837	3	AAA88520	Aaa88520 Human PRO
35	749.8	38.7	1837	3	AAAC58235	Aac58235 Human PRO
36	386.2	20.0	519	2	AAV35366	Aav35366 Human GDN
37	218.4	11.3	260	10	ACA55932	Aca55932 Human sig
38	218.4	11.3	260	12	ADI55728	Adi55728 Human pol
39	169.8	8.8	238	10	ACA55939	Aca55939 Mouse sig
40	169.8	8.8	238	12	ADI55735	Adi55735 Human pol
41	147	7.6	368	2	AAV99347	Aav99347 cDNA clon
42	103.4	5.3	521	13	ACF84889	Acf84889 Human SIR
43	102	5.3	1392	3	Aaz91456	Aaz91456 Human neu
44	102	5.3	1392	6	ABN87349	Abn87349 Human neu
45	102	5.3	1392	6	ABK50453	Abk50453 Human neu

ALIGNMENTS

RESULT 1

AAZ29100

ID AAZ29100 standard; cDNA; 1935 BP.

AC AAZ29100;

DT 07-FEB-2000 (first entry)

DE Murine GFRalpha3 cDNA.

KW Murine GFRalpha3; GFRalpha3; GFRalpha1;

glial-cell-line-derived neurotrophic factor family receptor alpha-3;

probe; homologous DNA; neuronal cell activation; GFRalpha3 ligand;

cell proliferation; cell differentiation; GFRalpha3-containing cell;

Ret-containing cell; peripheral nervous system disease; diabetes;

human immunodeficiency virus; chemotherapeutic agent treatment;

autonomic nervous system dysfunction; transgenic animal; ds.

XX Mus musculus.

XX Key Location/Qualifiers

XX CDS 89..1282

FT sig\_peptide /tag= a

FT /product= "Murine GFRalpha 3"

FT /tag= b

XX WO9949039-A2.

XX 30-SEP-1999.

XX 19-MAR-1999; 99WO-US06098.

XX 23-MAR-1998; 98US-0079124P.

XX 13-APR-1998; 98US-0081569P.

XX (GETH ) GENENTECH INC.

XX De Sauvage FJ, Klein RD, Phillips HS, Rosenthal A;

XX WPI; 2000-038358/03.

XX P-PSDB; AAY15174.

XX PT New isolated GPR-alpha3 nucleic acid, used to develop products for  
PT treating diseases or conditions involving peripheral nervous system or  
PT autonomic nervous system.  
XX PS  
XX PS Example 1; Fig 1; 112pp; English.  
CC The present sequence encodes full length mouse glial-cell-line-derived  
CC neurotrophic factor family receptor alpha-3 (GFRalpha3). This has  
CC sequence identity with GFRalpha1. GFRalpha3 DNA or its fragments can be  
CC used as a probe to screen for homologous DNA. GFRalpha3 possess neuronal  
CC cell activation property. GFRalpha3 ligands can be used to stimulate  
CC proliferation, growth, survival, differentiation, metabolism or  
CC regeneration of GFRalpha3- and Ret-containing cells. They can be useful  
CC in the treatment of peripheral nervous system diseases, eg. those  
CC associated with diabetes, human immunodeficiency virus, or  
CC chemotherapeutic agent treatments. Agonist or antagonists of GFRalpha3  
CC can be used to treat autonomic nervous system dysfunctions. The products  
CC can also be used for detection, diagnosis and production of transgenic  
CC animals  
XX SQ Sequence 1935 BP; 418 A; 584 C; 490 G; 443 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1935; DB 3; Length 1935;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1935; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTTGGCCCTCGAGGCGCAAGAAATTCGACAGCGGGGGGGCCCGAGGCGAGGAGC 60  
DB 1 GAAATTTGGCCCTCGAGGCGCAAGAAATTCGACAGCGGGGGGGCCCGAGGCGAGGAGC 60  
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DB 121 GCTGATGATCTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
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QY 1321 CCAGACTGATTTGAGGCTGTGGTGGGAGAACTGCGCAGCCTGTGGAAGAGAGCAGCAG 1380  
DB 1321 CCAGACTGATTTGAGGCTGTGGTGGGAGAACTGCGCAGCCTGTGGAAGAGAGCAGCAG 1380  
QY 1381 CGTGCTACAGCAACCCCGGAAACCAACAGGAGCTTCCGAGCAGCATCCCGTCTGCTCCAG 1440  
DB 1381 CGTGCTACAGCAACCCCGGAAACCAACAGGAGCTTCCGAGCAGCATCCCGTCTGCTCCAG 1440  
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DB 1441 AAGAGGCTCTTAGAAGTGAAGGCTGTGACCTTCCGATCTCAGCGGCTAGTTTTCAGAAC 1500  
QY 1501 TCCCTTGGCCCTGCTTCTTCTGCTCAGGCTGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1560  
DB 1501 TCCCTTGGCCCTGCTTCTTCTGCTCAGGCTGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1560  
QY 1561 TTTTGGCTTCTGCTGATGAGTGTAGCGGCTCACTTCCAGCGGCTTCTTCTGCTTCTTCTTCT 1620  
DB 1561 TTTTGGCTTCTGCTGATGAGTGTAGCGGCTCACTTCCAGCGGCTTCTTCTGCTTCTTCTTCT 1620  
QY 1621 AGGACCAACCCAGAGGCTAAGGAATCAGTCAATTCCTGTTGCTTCTTCCAGGAAGGCGAG 1680  
DB 1621 AGGACCAACCCAGAGGCTAAGGAATCAGTCAATTCCTGTTGCTTCTTCCAGGAAGGCGAG 1680  
QY 1681 TAAAGGTTTCTCAGGTTGACTGAGAAATATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1740  
DB 1681 TAAAGGTTTCTCAGGTTGACTGAGAAATATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1740  
QY 1741 TCCACAGTCCCTCTGATGAGAGATAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800  
DB 1741 TCCACAGTCCCTCTGATGAGAGATAAAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800



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QY 889 CCACGTGTCATCTCTATGACATCCTTTGGGACTTGTGCAACTGAGCAGTCCAGATGTCGCG 948
Db |||
QY 841 CCACGTGTCATCTCTATGACATCCTTTGGGACTTGTGCAACTGAGCAGTCCAGATGTCGCG 900
Db |||
QY 949 GGCATACCTGGGGCTGATTGGGACTGTCATGACCCCAAACTTTCATCAGAAAGGTCAACAC 1008
Db |||
QY 901 GGCATACCTGGGGCTGATTGGGACTGTCATGACCCCAAACTTTCATCAGAAAGGTCAACAC 960
QY 1009 TACTGTTGCTTAAGCTGACCTCGCGAGGAGCGCACTTACAGGAGGAGTGTGAACA 1068
Db |||
QY 961 TACTGTTGCTTAAGCTGACCTCGCGAGGAGCGCACTTACAGGAGGAGTGTGAACA 1020
Db |||
QY 1069 GCTGAAAGGTCTCTTCTCCAGAACCTCTGCTGAGGAGGCAATGAGGAGTGAAGTGG 1128
Db |||
QY 1021 GCTGAAAGGTCTCTTCTCCAGAACCTCTGCTGAGGAGGCAATGAGGAGTGAAGTGG 1080
QY 1129 TTTCCACAGACAGCTCTTCTCCAGAGCTGGGACAGCTCTACTTTTTCAGTGGTGACGA 1188
Db |||
QY 1081 TTTCCACAGACAGCTCTTCTCCAGAGCTGGGACAGCTCTACTTTTTCAGTGGTGACGA 1140
QY 1189 GCAGAACAGCAACCTCTCTGAGACTGAGGAGGCTACCCATCTCTTCTTCTCCAT 1248
Db |||
QY 1141 GCAGAACAGCAACCTCTCTGAGACTGAGGAGGCTACCCATCTCTTCTTCTCCAT 1200
QY 1249 CCTTCCCTTGATTCTGCTGCAGACCTCTGCTGAGCTGGGCTTCTCAGGCTCTTGTGCC 1308
Db |||
QY 1201 CCTTCCCTTGATTCTGCTGCAGACCTCTGCTGAGCTGGGCTTCTCAGGCTCTTGTGCC 1260
QY 1309 TCTCCACACACCCAGACTGATTTTTCAGCCTGTGTGGGAGAGAACTCGCCAGCCTGTGG 1368
Db |||
QY 1261 TCTCCACACACCCAGACTGATTTTTCAGCCTGTGTGGGAGAGAACTCGCCAGCCTGTGG 1320
QY 1369 AAGAGAGCAGCGTGTCTACAGCAACCCGGAACCAACAGGCAATTCGAGCAGCAATCC 1428
Db |||
QY 1321 AAGAGAGCAGCGTGTCTACAGCAACCCGGAACCAACAGGCAATTCGAGCAGCAATCC 1380
QY 1429 CQTCTGCTCCAGAGAGGTCTTGTAGAGTGAAGGCTGTGACCTTCCGATCCTGAGCGGT 1488
Db |||
QY 1381 CQTCTGCTCCAGAGAGGTCTTGTAGAGTGAAGGCTGTGACCTTCCGATCCTGAGCGGT 1440
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Db |||
QY 1441 AGTTTTCAAAACCTCCTTGTGCCCTCTCTTCTGCTCAGGCTCCTCTCTTCTTGGACT 1500
QY 1549 TTGTGGTCCAGTTTGTGCTCTGCTGATGAGGCTCAGGCTCAGGCTCAGGCTCAGGCTC 1608
Db |||
QY 1501 TTGTGGTCCAGTTTGTGCTCTGCTGATGAGGCTCAGGCTCAGGCTCAGGCTCAGGCTC 1560
QY 1609 TTCTGTTTCCAGGACCAACCCAGAGGCTTAAGGAATCAGTCAATTCCTGTTGCTTCTTCC 1668
Db |||
QY 1561 TTCTGTTTCCAGGACCAACCCAGAGGCTTAAGGAATCAGTCAATTCCTGTTGCTTCTTCC 1620
QY 1669 AGGAAGGAGGCTTAAGGTTCTGAGGTGATGAGAAATGTTTCTTGTGTGGAAGGC 1728
Db |||
QY 1621 AGGAAGGAGGCTTAAGGTTCTGAGGTGATGAGAAATGTTTCTTGTGTGGAAGGC 1680
QY 1729 TGTGCTCCAGCTCAGCTCCTCTGATGAGAAATGTTTCTTGTGTGGAAGGC 1788
Db |||
QY 1681 TGTGCTCCAGCTCAGCTCCTCTGATGAGAAATGTTTCTTGTGTGGAAGGC 1740
QY 1789 GCTCTGCCAGGCAATCTCGAAATTTGGGATGAGAGCTTAAGTCTTGGGTCTTGTGT 1848
Db |||
QY 1741 GCTCTGCCAGGCAATCTCGAAATTTGGGATGAGAGCTTAAGTCTTGGGTCTTGTGT 1800
QY 1849 AACTCCTATTACTGTCCCAAAATTCCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1908
Db |||
QY 1801 AACTCCTATTACTGTCCCAAAATTCCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1860
QY 1909 TTAATAAAAAAAAAAAAAAAAAAAAAA 1935
Db |||
QY 1861 TTAATAAAAAAAAAAAAAAAAAAAAAA 1887
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RESULT 3
ID ADJ58708 standard; cDNA; 1889 BP.
XX
AC ADJ58708;
XX
DT 06-MAY-2004 (first entry)
XX
DE Murine retL3 cDNA.
XX
KW Tissue growth; retL protein; organ failure; foetal malformation;
tumour growth; renal tissue; cytostatic; vulnery; nephrotropic; murine;
gene; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
CDS 41..1234
FT /*tag= a
FT /product= "Murine retL3 protein"
XX
XX US6677135-B1.
XX
PD 13-JAN-2004.
XX
XX 06-NOV-1998; 98US-00187906.
XX
XX 08-MAY-1996; 96US-0017427P.
XX 07-JUN-1996; 96US-0019300P.
XX 16-JUL-1996; 96US-0021859P.
XX 23-AUG-1996; 96US-0023444P.
XX 11-APR-1997; 97US-0043533P.
XX 07-MAY-1997; 97WO-US007726.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;
XX
XX WPI; 2004-079845/08.
XX P-FSDB; ADJ58709.
XX
XX New nucleic acid encoding Ret polypeptide, useful for diagnosing and/or
treating diseases or conditions associated with aberrant expression or
activity of the Ret ligand, such as organ failure, fetal malformations
and tumor growth.
XX
XX Claim 3; SEQ ID NO 16; 66pp; English.
XX
XX The present invention relates to nucleotide and amino acid sequences
which promote tissue growth and methods for modulating tissue growth. The
invention also relates to retL proteins and polynucleotides encoding such
proteins. RetL proteins interact with a receptor protein Ret to trigger
dimerisation and/or autophosphorylation of the tyrosine kinase domain of
the receptor protein Ret. The methods and compositions of the present
invention are useful for the diagnosis and/or treatment of diseases or
conditions associated with aberrant expression or activity of the Ret
ligand, such as organ failure, foetal malformations and tumour growth and
for promoting regeneration or survival of damaged renal tissue. The
present sequence is murine retL3 cDNA of the invention.
XX
SQ Sequence 1889 BP; 410 A; 569 C; 473 G; 437 T; 0 U; 0 Other;
Query Match 97.5%; Score 1887; DB 12; Length 1889;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 CGCAGGAGAGGCGTGTGCGATCCCGGCGTCCACCCGCCATGGGGCTCTCTCTGGAGCCC 108
Db 1 CGCAGGAGAGGCGTGTGCGATCCCGGCGTCCACCCGCCATGGGGCTCTCTCTGGAGCCC 60
QY 109 GCGACCTCCACTGCTGATGATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 168
Db 61 GCGACCTCCACTGCTGATGATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
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QY 169 AGGAAATCCCTTGGCCACAGAGAAACAGGTTTGTGAACAGCTGTATCCAGGCGCAGAAAGAA 228
Db 121 AGGAAATCCCTTGGCCACAGAGAAACAGGTTTGTGAACAGCTGTATCCAGGCGCAGAAAGAA 180
QY 229 ATGCGAGGCTAATCCGGCTTGAAGGCTGCTTACAGCAACCTGGGCTCTGTGACCTCCAG 288
Db 181 ATGCGAGGCTAATCCGGCTTGAAGGCTGCTTACAGCAACCTGGGCTCTGTGACCTCCAG 240
QY 289 TTTAAGCAGGCGCTGCTTACAGAGAGTCTGCCATGCTGACAGACTGCTAGAGGAGC 348
Db 241 TTTAAGCAGGCGCTGCTTACAGAGAGTCTGCCATGCTGACAGACTGCTAGAGGAGC 300
QY 349 AGAAACAATCAGAAACAGCTCTCTATAGACTGCAAGTGCATCGCGCATGAAGACCA 408
Db 301 AGAAACAATCAGAAACAGCTCTCTATAGACTGCAAGTGCATCGCGCATGAAGACCA 360
QY 409 AGCTACCTGTCTGGACATTTATGGACCGTTTACACCTGCCGAGCGCTTGGTACTAGA 468
Db 361 AGCTACCTGTCTGGACATTTATGGACCGTTTACACCTGCCGAGCGCTTGGTACTAGA 420
QY 469 GTTGGATGTCTCACCTATGAAGACACAGTGAACAGCAACCTCGAAATGAATCTTAG 528
Db 421 GTTGGATGTCTCACCTATGAAGACACAGTGAACAGCAACCTCGAAATGAATCTTAG 480
QY 529 CAAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCCCTCAAAATTTGCTGTGTAC 588
Db 481 CAAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCCCTCAAAATTTGCTGTGTAC 540
QY 589 TCTTACAGCAAGTGTGACCGCTCGGCAAGGCTTACGGGAGGATGCTCAGGGATCCG 648
Db 541 TCTTACAGCAAGTGTGACCGCTCGGCAAGGCTTACGGGAGGATGCTCAGGGATCCG 600
QY 649 CTGCGAGCGCACCTCTGCTAGCCAGCTGGCTCTTCTTGAAGAGGAGCAGAGATC 708
Db 601 CTGCGAGCGCACCTCTGCTAGCCAGCTGGCTCTTCTTGAAGAGGAGCAGAGATC 660
QY 709 CCACGCTCAGGGTCTGCTGTGTCTCTGTGTCACAGAGATGCGGGCTGTGGGAGCG 768
Db 661 CCACGCTCAGGGTCTGCTGTGTCTCTGTGTCACAGAGATGCGGGCTGTGGGAGCG 720
QY 769 GGGGGTAAACACCATCGCCCCAGTTGGCCCTGCTCTGTAAACCCCAATTTGCTGGA 828
Db 721 GGGGGTAAACACCATCGCCCCAGTTGGCCCTGCTCTGTAAACCCCAATTTGCTGGA 780
QY 829 TCTGCGGAGCTTCTGCGGTGGGAGCCCTTTGTGACAGATCAGCCCTGATGGACTCCAGAC 888
Db 781 TCTGCGGAGCTTCTGCGGTGGGAGCCCTTTGTGACAGATCAGCCCTGATGGACTCCAGAC 840
QY 889 CCACCTGTCTATCTATGACATCCTTTGGGACTTGTGCAACTGAGCAGTCCAGATGTCTCG 948
Db 841 CCACCTGTCTATCTATGACATCCTTTGGGACTTGTGCAACTGAGCAGTCCAGATGTCTCG 900
QY 949 GGCATACCTGGGGCTGATTTGGAGTGCATGATGCCCAAACTTCATCAGCAGGTCAACAC 1008
Db 901 GGCATACCTGGGGCTGATTTGGAGTGCATGATGCCCAAACTTCATCAGCAGGTCAACAC 960
QY 1009 TACTGTTCCTTAAAGCTGACCTGCGAGGAGCGGCAACCTTACAGGACGAGTGTGAACA 1068
Db 961 TACTGTTCCTTAAAGCTGACCTGCGAGGAGCGGCAACCTTACAGGACGAGTGTGAACA 1020
QY 1069 GCTGAAAGGCTCTTCTCCAGAAACCCCTGCTCGTGGAGGCCATTTGAGCTAAGATCGG 1128
Db 1021 GCTGAAAGGCTCTTCTCCAGAAACCCCTGCTCGTGGAGGCCATTTGAGCTAAGATCGG 1080
QY 1129 TTTTCCACAGACAGCTCTTCTCCAGAGCTGGGACAGCTCTACTTTTTTTCAGTGTGACGA 1188
Db 1081 TTTTCCACAGACAGCTCTTCTCCAGAGCTGGGACAGCTCTACTTTTTTTCAGTGTGACGA 1140
QY 1189 GCAGAACAGCAACCTCTGAGACTGCGCCAGGCTACCCATTTCTTTCTTCTCCAT 1248
Db 1141 GCAGAACAGCAACCTCTGAGACTGCGCCAGGCTACCCATTTCTTTCTTCTCCAT 1200
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QY 1249 CTTTCCCTTGATTTCTGTGACAGACCTCTGTGTAGCTGGGCTTCTCTCAGGGTCTTTGTTC 1308
Db 1201 CTTTCCCTTGATTTCTGTGACAGACCTCTGTGTAGCTGGGCTTCTCTCAGGGTCTTTGTTC 1260
QY 1309 TCTCCACACACACAGCTGATTTGCAAGCTGTGTGGGAGAGAACTCGCCAGCCTGTGG 1368
Db 1261 TCTCCACACACACAGCTGATTTGCAAGCTGTGTGGGAGAGAACTCGCCAGCCTGTGG 1320
QY 1369 AAGAAGACGCAAGCTGTCTACACAGCAACCCGGAAACCAACCAAGGCAATTCGCGAGCAATCC 1428
Db 1321 AAGAAGACGCAAGCTGTCTACACAGCAACCCGGAAACCAACCAAGGCAATTCGCGAGCAATCC 1380
QY 1429 CGTCTGCTCCAGAGAGGCTCTTAGAGTGAAGGCTGTGACCCCTTCGATCTCAGAGCGCT 1488
Db 1381 CGTCTGCTCCAGAGAGGCTCTTAGAGTGAAGGCTGTGACCCCTTCGATCTCAGAGCGCT 1440
QY 1489 AGTTTTCACAACTCCCTTGGCCCTGCTTCTTCTGGCTCAGGCTGCTCTCTCTAGGACT 1548
Db 1441 AGTTTTCACAACTCCCTTGGCCCTGCTTCTTCTGGCTCAGGCTGCTCTCTCTAGGACT 1500
QY 1549 TTGTGGTCCAGTTTTCCTTCTGTCTGTATGGTGTATAGCGGCTCACTCCAGCGCTTC 1608
Db 1501 TTGTGGTCCAGTTTTCCTTCTGTCTGTATGGTGTATAGCGGCTCACTCCAGCGCTTC 1560
QY 1609 TTCTGTCTTCCAGAGACCAACCCAGAGGCTAAGGAATCAGTCAATTCCTCTGTGCTTCTTC 1668
Db 1561 TTCTGTCTTCCAGAGACCAACCCAGAGGCTAAGGAATCAGTCAATTCCTCTGTGCTTCTTC 1620
QY 1669 AGGAAGCAGGCTAAGGGTCTGAGGTGACCTGAGAAATGTTTCTTGTGTGGAAGGC 1728
Db 1621 AGGAAGCAGGCTAAGGGTCTGAGGTGACCTGAGAAATGTTTCTTGTGTGGAAGGC 1680
QY 1729 TGGTGTCTCCAGCTTCCAGCTCCCTCTGAATGGAAAGATAAAACCTGTGTGTCTTGAAT 1788
Db 1681 TGGTGTCTCCAGCTTCCAGCTCCCTCTGAATGGAAAGATAAAACCTGTGTGTCTTGAAT 1740
QY 1789 GCTTGCAGGCAATCTGAAACATTTGGGCAATGAAGAGCTAAAGTCTTTGGGTCTTGTTT 1848
Db 1741 GCTTGCAGGCAATCTGAAACATTTGGGCAATGAAGAGCTAAAGTCTTTGGGTCTTGTTT 1800
QY 1849 AACTCTTATTTACTGCTCCCAATTTCCCTAGTCTCCCTTGGGTCTATGATTAACATTTTGCAC 1908
Db 1801 AACTCTTATTTACTGCTCCCAATTTCCCTAGTCTCCCTTGGGTCTATGATTAACATTTTGCAC 1860
QY 1909 TTAATAAAAAAAAAAAAAAAAAAAAAA 1935
Db 1861 TTAATAAAAAAAAAAAAAAAAAAAAAA 1887

RESULT 4
ADY53844
ID ADY53844 standard; cDNA; 1889 BP.
XX
AC ADY53844;
XX
DT 05-MAY-2005 (first entry)
XX
DE Mouse retL3 cDNA.
XX
KW DNA purification; immune stimulation; ret ligand; gene; ss.
XX
OS Mus sp.
XX
PN US6861509-B1.
XX
PD 01-MAR-2005.
XX
PF 21-JAN-2000; 2000US-00489407.
XX
PR 08-MAY-1996; 96US-0017427P.
PR 07-JUN-1996; 96US-0019300P.
PR 16-JUL-1996; 96US-0021859P.
PR 23-AUG-1996; 96US-0023444P.
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Db 1741 GCTCTGCCAGGCAATCTGAAACATTTGGGCATGAAGAGCTAAAGTCTTTGGGTCTTGTTT 1800  
QY 1849 AACTCTATTACTGTCTCCCAATTCCTTCCCTAGTCCCTTGGGTCTGATTAACATTTTGAC 1908  
Db 1801 AACTCTATTACTGTCTCCCAATTCCTTCCCTAGTCCCTTGGGTCTGATTAACATTTTGAC 1860  
QY 1909 TTAATAAAAAAAAAAAAAAAAAAAAAA 1935  
Db 1861 TTAATAAAAAAAAAAAAAAAAAAAAAA 1887

RESULT 5  
ADZ00208  
ID ADZ00208 standard; cDNA; 1889 BP.  
XX  
AC ADZ00208;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Mouse Ret ligand 3 (RetL3)-encoding cDNA, SEQ ID NO:16.  
XX  
KW Cell growth; development; signal transduction; neurological disease;  
KW renal disease; genitourinary disease; neuroprotective; nephrotropic;  
KW cancer; neoplasm; cytosolic; RetL3;  
KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;  
KW GDNF family receptor alpha 3; GFRA3; gene; ss.  
XX  
OS Mus sp.

XX  
FH Key Location/Qualifiers  
FT CDS 41..1234  
FT /\*tag= a  
FT /product= "RetL3"  
XX  
XX US2005080235-A1.  
XX  
PD 14-APR-2005.  
XX  
XX 23-SEP-2003; 2003US-00668936.  
XX  
PR 08-MAY-1996; 96US-0017427P.  
PR 07-JUN-1996; 96US-0019300P.  
PR 16-JUL-1996; 96US-0021859P.  
PR 23-AUG-1996; 96US-0023444P.  
PR 11-APR-1997; 97US-0043533P.  
PR 07-MAY-1997; 97WO-US007726.  
PR 06-NOV-1998; 98US-00187906.  
XX

XX (SANI/) SANICOLA-NADEL M.  
XX (HESS/) HESSION C.  
XX (CATE/) CATE R L.  
XX (WORL/) WORLEY D S.  
XX  
XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;  
XX  
XX WPI; 2005-305025/31.  
XX P-PSDB; ADZ00209.  
XX  
XX New polypeptide sequence that interacts with a receptor protein Ret to  
XX trigger dimerization or autophosphorylation, useful in preparing a  
XX composition for treating neurodegenerative disorders, e.g., Alzheimer's  
XX disease.  
XX  
XX Disclosure; SEQ ID NO 16; 67pp; English.

XX  
XX The invention relates to the murine and human RetL3 (Ret ligand 3)  
XX proteins (ADZ00209 and ADZ00213, respectively) and to proteins at least  
XX 80% identical to murine or human RetL3. The invention also discloses  
XX other RetL proteins such as rat RetL1, human RetL1, human RetL2,  
XX fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences  
XX encoding these RetL proteins or protein fragments. Like other RetL  
XX proteins, the RetL3 proteins of the invention interact with the Ret  
XX receptor tyrosine kinase that is encoded by the Ret proto-oncogene,  
XX

CC triggering Ret receptor dimerization or autophosphorylation. The Ret  
CC receptor is expressed during development in a variety of tissues,  
CC including the peripheral and central nervous systems and the kidney. It  
CC is also expressed in some cancers. RetL proteins such as the murine and  
CC human RetL3 proteins, and RetL polynucleotides may be used for  
CC stimulating Ret receptor signaling, thereby promoting renal or neuronal  
CC cell growth or survival and minimizing damage to such tissues after  
CC various insults. They may therefore be used to treat renal disorders  
CC (e.g., renal failure, renal tube defects and renal trauma) or  
CC neurological disorders including neurodegenerative disorders (e.g.,  
CC Alzheimer's disease), bacterial or viral diseases of the nervous system  
CC (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage  
CC or trauma) and developmental neural disorders (e.g., mental retardation).  
CC Conversely, antibodies against RetL may be used to block RetL-Ret  
CC receptor signal transduction for inhibiting tumor growth, fusion proteins  
CC comprising a RetL protein are useful for targeting a drug to Ret receptor  
CC -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may  
CC also be used in medical imaging. The present sequence represents a full-  
CC length murine RetL3 cDNA isolated in the invention.  
XX

XX  
SQ Sequence 1889 BP; 410 A; 569 C; 473 G; 437 T; 0 U; 0 Other;  
Query Match 97.5%; Score 1887; DB 14; Length 1889;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 49 CGCAGGCAGAGCGTGTGCGATCCCGGCGCTCCACCCGCCATGGGGTCTCTCTGGAGCCC 108  
Db 1 CGCAGGCAGAGCGTGTGCGATCCCGGCGCTCCACCCGCCATGGGGTCTCTCTGGAGCCC 60  
QY 109 CGGACCTCCACTGCTGATGATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 168  
Db 61 CGGACCTCCACTGCTGATGATCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
QY 169 AGGAACTCCCTTCCACAGAGAAACAGTTTGTGAACAGCTGTACCCAGGCCAGAAAGAA 228  
Db 121 AGGAACTCCCTTCCACAGAGAAACAGTTTGTGAACAGCTGTACCCAGGCCAGAAAGAA 180  
QY 229 ATGCGAGGCTAATCCCGCTTGCAGAGGCTGCCTACAGCACCTGGGCTCTCTGCACCTCCAG 288  
Db 181 ATGCGAGGCTAATCCCGCTTGCAGAGGCTGCCTACAGCACCTGGGCTCTCTGCACCTCCAG 240  
QY 289 TTTAAGCAGGCGCTGCCCTTAGAGGAGTCTGCCATGCTGCAGACTGCCTTAGAGGCGAGC 348  
Db 241 TTTAAGCAGGCGCTGCCCTTAGAGGAGTCTGCCATGCTGCAGACTGCCTTAGAGGCGAGC 300  
QY 349 AGAACAACTCAGGAACAGCTCTCTGTAGTAGCTGAGGCTGCCATCGGGCATGAGACCA 408  
Db 301 AGAACAACTCAGGAACAGCTCTCTGTATAGACTGAGGCTGCCATCGGGCATGAGACCA 360  
QY 409 AGCTACCTGTCTGGACATTTATTGGACCGTTTACCCCTCCCGAAGCCCTTGGTACTACGA 468  
Db 361 AGCTACCTGTCTGGACATTTATTGGACCGTTTACCCCTCCCGAAGCCCTTGGTACTACGA 420  
QY 469 GTTGGATGTCTCACCCCTATGAAGACACAGTGACACAGCAAAACCTCGGAAAATGAATCTTAG 528  
Db 421 GTTGGATGTCTCACCCCTATGAAGACACAGTGACACAGCAAAACCTCGGAAAATGAATCTTAG 480  
QY 529 CAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCTCAAAATTTGCTATGCTGTATAC 588  
Db 481 CAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCTCAAAATTTGCTATGCTGTATAC 540  
QY 589 TCTTCACGACAAAGTGTGACCCGCTCGCAAGGCCCTACGGGGAGGAGCATGCTCAGGGATCCG 648  
Db 541 TCTTCACGACAAAGTGTGACCCGCTCGCAAGGCCCTACGGGGAGGAGCATGCTCAGGGATCCG 600  
QY 649 GTGCGAGGCGCACCTTGTGCTTAGCCAGCTGCGCTCTCTTTTGAAGAGGAGGAGGAGTTC 708  
Db 601 GTGCGAGGCGCACCTTGTGCTTAGCCAGCTGCGCTCTCTTTTGAAGAGGAGGAGGAGTTC 660  
QY 709 CCAGCTCAGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768  
Db 661 CCAGCTCAGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720



Db	1	CGCGCGCCGACGCGCAGCGCGCTGTGCGATCCGCGCGCTCCACCCGCCATGGGGCT	60
Qy	97	CTCCTGAGCCCGGCACTCTCACCTGCTGATGATCCTCTACTCTGATGCTGTGCTGTGTGGCT	156
Db	61	CTCTGAGCCCGGCACTCTCCATGCTGATGATCCTCTACTCTGCTGTGTGTGTGGCT	120
Qy	157	GCCATTGGAGCAGGAACTCCCTTGGCCACAGAGAACAGGTTTGTGAACAGCTGTACCCA	216
Db	121	GCCACTTGGAGCAGAACTCCCTTGGCCACAGAGAACAGGTTTGTGAACAGCTGTACCCA	180
Qy	217	GGCCAGAAAGAAATGCGAGGCTAATCCGCTTGCAGGCTGCCCTTACAGCAACTGGGCTC	276
Db	181	GGCCAGAAAGAAATGCGAGGCTAATCCGCTTGCAGGCTGCCCTTACAGCAACTGGGCTC	240
Qy	277	CTGCACCTCAGATTAAAGCAGGCGCTGCCCTCTAGAGAGTCTGTGCCATGTCTGCAGACTG	336
Db	241	CTGCACCTCAG-TTAAGCAGGCGCTGCCCTCTAGAGAGTCTGTGCCATGTCTGCAGACTG	299
Qy	337	CCTAGAGGCAGAGAAACAACTCAGGAAACAGCTCTCTGATAGACTGCGAGTGCATCGGCG	396
Db	300	CCTAGAGGCAGAGAAACAACTCAGGAAACAGCTCTCTGATAGACTGCGAGTGCATCGGCG	359
Qy	397	CATGAAGCACAGACTACCTGTCTGGACATTTATTGSAACGTTTCACTCTGCCCGAAGCCT	456
Db	360	CATGAAGCACAGACTACCTGTCTGGACATTTATTGSAACGTTTCACTCTGCCCGAAGCCT	419
Qy	457	TGCTGACTACGAGTTGGATGCTCACCCCTATGAAGACACAGTGCAGCAGCAAAACCTGGAA	516
Db	420	TGCTGACTACGAGTTGGATGCTCACCCCTATGAAGACACAGTGCAGCAGCAAAACCTGGAA	479
Qy	517	AATGAATCTTTAGCAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCCTCAAAATTGC	576
Db	480	AATGAATCTTTAGCAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCCTCAAAATTGC	539
Qy	577	TATGCTGTGTACTTTCCAGCAAGTGTGACCGCTGCGCAAGGCTTACGGGAGGCGATG	636
Db	540	TATGCTGTGTACTTTCCAGCAAGTGTGACCGCTGCGCAAGGCTTACGGGAGGCGATG	599
Qy	637	CTCAGGGATCCGCTGCCAGCGCACCTCTGCCTAGCCACAGCTCGGCTCTCTTTTGAGAA	696
Db	600	CTCAGGGATCCGCTGCCAGCGCACCTCTGCCTAGCCACAGCTCGGCTCTCTTTTGAGAA	659
Qy	697	GGCAGCAGAGTCCACGCTCAGGGTCTGCTGTCTGTCTGTCACACAGAGATGCGGG	756
Db	660	GGCAGCAGAGTCCACGCTCAGGGTCTGCTGTCTGTCTGTCACACAGAGATGCGGG	719
Qy	757	CTGTGGGAGCGGCGGTAAACCATGCGCCCCAGTGTGCGCCCTGCTTCTGTAAACCC	816
Db	720	CTGTGGGAGCGGCGGTAAACCATGCGCCCCAGTGTGCGCCCTGCTTCTGTAAACCC	779
Qy	817	CAATTGCTGGATCTGCGGAGCTTCTGCTGCGGACCCCTTGTGAGATCAGCCTGAT	876
Db	780	CAATTGCTGGATCTGCGGAGCTTCTGCTGCGGACCCCTTGTGAGATCAGCCTGAT	839
Qy	877	GGACTTCCAGACCCACATGTCACTCTATGGACATCTTGGGACTTGTGCAACTCAGCAGTC	936
Db	840	GGACTTCCAGACCCACATGTCACTCTATGGACATCTTGGGACTTGTGCAACTCAGCAGTC	899
Qy	937	CAGATGTCGTGCGGCATACCTGGGGCTGATTGGGACTGCCATGACCCCAAACTTCATCAG	996
Db	900	CAGATGTCGTGCGGCATACCTGGGGCTGATTGGGACTGCCATGACCCCAAACTTCATCAG	959
Qy	997	CAAGGTCAACACTACTGTTGGCTTAAAGTGTCACTGCGGAGGCGGCAACCTACAGGA	1056
Db	960	CAAGGTCAACACTACTGTTGGCTTAAAGTGTCACTGCGGAGGCGGCAACCTACAGGA	1019
Qy	1057	CGAGTGTGAACAGCTGGAAGGTCTTCTCCAGAACCTCTGCTCGTGAGGCGCATTCG	1116
Db	1020	CGAGTGTGAACAGCTGGAAGGTCTTCTCCAGAACCTCTGCTCGTGAGGCGCATTCG	1079
Qy	1117	AGCTTAAGATCGTTTCCACAGACAGCTCTTCTCCAGGACTGGGCGAGCTCTACTTTTC	1176

Db	1080	AGCTAAGATGGGTTTCCACAGACAGCTCTTCTCCAGGACTGGGACAGACTCTACTTTTTC	1133
Qy	1177	AGTGGTGCAGCAGCAGAAACCCCTGCTCTGAGACTGCAGCCACAGGCTACCCATTTCT	1236
Db	1140	AGTGGTGCAGCAGCAGAAACCCGCTCTCTGAGACTGCAGCCACAGGCTACCCATTTCT	1199
Qy	1237	TTCTTTTCCATCCTTCCCTTGAATTCGTGACAGCCCTCTGTAGCTGGGCTTCCTCAG	1296
Db	1200	TTCTTTTCCATCCTTCCCTTGAATTCGTGACAGCCCTCTGTAGCTGGGCTTCCTCAG	1259
Qy	1297	GGTCCTTTGTGCTCTCCACACACCCAGACTGATTTGACGCTGTGTGGGAGAGAACTC	1356
Db	1260	GGTCCTTTGTGCTCTCCACACACCCAGACTGATTTGACGCTGTGTGGGAGAGAACTC	1319
Qy	1357	GCCAGCCTGTGGAGAAAGACGCGGTGTCTACACAGCAACCCGAAACCAACAGGCAATTC	1416
Db	1320	GCCAGCCTGTGGAGAAAGACGCGGTGTCTACACAGCAACCCGAAACCAACAGGCAATTC	1379
Qy	1417	CGAGACATCCCGTCTGCTCTCAGAGAGAGTCTTAGAGTGAAGGCTGTGACCCCTTCCGA	1476
Db	1380	CGAGACATCCCGTCTGCTCTCAGAGAGAGTCTTAGAGTGAAGGCTGTGACCCCTTCCGA	1439
Qy	1477	TCCTGAGCGGTAGTTTTCAAACCTCCCTTGCCCTGCTTCTTCTGGCTCAGGCTGCTC	1536
Db	1440	TCCTGAGCGGTAGTTTTCAAACCTCCCTTGCCCTGCTTCTTCTGGCTCAGGCTGCTC	1499
Qy	1537	CTCCCTTAGGACTTTGTGGGTCCAGATTTTGCTTCTGTTCTGATGGTGATTTAGCGGCTCAC	1596
Db	1500	CTCCCTTAGGACTTTGTGGGTCCAGATTTTGCTTCTGTTCTGATGGTGATTTAGCGGCTCAC	1559
Qy	1597	CTCAGCGCTTCTTCTGTTTCCAGGACCAACCCAGAGGCTAAGGAATCAGTCATTTCCCT	1656
Db	1560	CTCAGCGCTTCTTCTGTTTCCAGGACCAACCCAGAGGCTAAGGAATCAGTCATTTCCCT	1619
Qy	1657	GTTCGCTTCTCCAGGAAGGCAAGGCTAAGGTTCTGAGTGCACTGAGAAAATGTTTCCCTT	1716
Db	1620	GTTCGCTTCTCCAGGAAGGCAAGGCTAAGGTTCTGAGTGCACTGAGAAAATGTTTCCCTT	1679
Qy	1717	TGTTGGAAGGCTGGTCTCTCAGCCTCCAGTCCCTCTGTAATGGAAGATAAAAACCTGCT	1776
Db	1680	TGTTGGAAGGCTGGTCTCTCAGCCTCCAGTCCCTCTGTAATGGAAGATAAAAACCTGCT	1739
Qy	1777	GGTGTCTTGACTGCTCTGCCAGGCAATCTGAAACATTTGGGCAATGAAGACTTAAGTCTT	1836
Db	1740	GGTGTCTTGACTGCTCTGCCAGGCAATCTGAAACATTTGGGCAATGAAGACTTAAGTCTT	1799
Qy	1837	TGGGTCTTGTTTAACCTCTATTACTGTCCCAAAATTCCTCTGCTGGGTCATGATTT	1896
Db	1800	TGGGTCTTGTTTAACCTCTATTACTGTCCCAAAATTCCTCTGCTGGGTCATGATTT	1859
Qy	1897	AAACATTTTGACTTAAAAA 1915	
Db	1860	AAACATTTTGACTTAAAAA 1878	
RESULT 7			
ID	ADJ58706	standard; cdna; 1878 BP.	
XX	AC		
XX	ADJ58706;		
DT	06-MAY-2004	(first entry)	
XX	Murine retL3 partial cdna.		
XX			
KW	Tissue growth; retL protein; organ failure; foetal malformation;		
KW	tumour growth; renal tissue; cytotstatic; vulnery; nephrotropic; murine;		
KW	gene; ss.		
XX			
OS	Mus sp.		
XX			
Key	Location/Qualifiers		
FH	205..1245		
CDS			



QY 1477 TCGTAGCGGCTAGTTTCAAACTCCCTTGGCCCTGCTTCTTCTGCTCAGGCTGCTC 1536  
DB 1440 TCGTAGCGGCTAGTTTCAAACTCCCTTGGCCCTGCTTCTTCTGCTCAGGCTGCTC 1499  
QY 1537 CTCCTTAGGACTTTGGGCTCAGTTTGGCCCTTCTGTTCTGATGCTGATTAGCGGCTCAG 1596  
DB 1500 CTCCTTAGGACTTTGGGCTCAGTTTGGCCCTTCTGTTCTGATGCTGATTAGCGGCTCAG 1559  
QY 1597 CTCAGCGCTTCTTCTGTTTCCAGGACCAACCCAGAGGCTAAGGAATCAGTCAATTCCT 1656  
DB 1560 CTCAGCGCTTCTTCTGTTTCCAGGACCAACCCAGAGGCTAAGGAATCAGTCAATTCCT 1619  
QY 1657 GTTGCTTCTCAGGAGCAGGCTAAGGTTCTGAGGTGACTGAGAAAAATGTTTCTT 1716  
DB 1620 GTTGCTTCTCAGGAGCAGGCTAAGGTTCTGAGGTGACTGAGAAAAATGTTTCTT 1679  
QY 1717 TGTGTGGAAGGCTGCTGCTCCAGGCTCCACGTCCTCTGAAATGGAAGATAAAAACTGCT 1776  
DB 1680 TGTGTGGAAGGCTGCTGCTCCAGGCTCCACGTCCTCTGAAATGGAAGATAAAAACTGCT 1739  
QY 1777 GGTGTCTTGAAGCTGCTGCTCCAGGCAATCTGAAACATTTTGGGCATGAAGAGCTTAAAGTCTT 1836  
DB 1740 GGTGTCTTGAAGCTGCTGCTCCAGGCAATCTGAAACATTTTGGGCATGAAGAGCTTAAAGTCTT 1799  
QY 1837 TGGGTCTTGTAACTTCTTAACTGCTGCTCCAAATTCCTGAGTCCCTTGGGTCAATGATT 1896  
DB 1800 TGGGTCTTGTAACTTCTTAACTGCTGCTCCAAATTCCTGAGTCCCTTGGGTCAATGATT 1859  
QY 1897 AAACATTTGACTTAAAAA 1915  
DB 1860 AAACATTTGACTTAAAAA 1878

## RESULT 8

ADY53842

ID ADY53842 standard; cDNA; 1878 BP.

XX

AC ADY53842;

XX

DT 05-MAY-2005 (first entry)

XX

DE Partial mouse retL3 cDNA.

XX

KW DNA purification; immune stimulation; ret ligand; gene; ss.

XX

OS Mus sp.

XX

PN US6861509-B1.

XX

PD 01-MAR-2005.

XX

PF 21-JAN-2000; 2000US-00489407.

XX

PR 08-MAY-1996; 96US-0017427P.

XX

PR 07-JUN-1996; 96US-0019300P.

XX

PR 16-JUL-1996; 96US-0021859P.

XX

PR 23-AUG-1996; 96US-0023444P.

XX

PR 11-APR-1997; 97US-0043533P.

XX

PR 07-MAY-1997; 97MO-US007726.

XX

PR 06-NOV-1998; 98US-00187906.

XX

PA (BIOJ ) BIOGEN INC.

XX

PI Sanicola-Nadel M, Hession C, Cate RL, Worley DS;

XX

DR WPI; 2005-201184/21.

XX

DR P-PSDB; ADY53843.

XX

PT New anti-ret ligand (RetL) antibody, useful for treating acute renal

XX

PT failure, acute nephritis, chronic renal failure, nephritic syndrome, as

XX

PT well as Alzheimer's disease, Parkinson's and multiple sclerosis.

XX

PS Disclosure; SEQ ID NO 14; 66pp; English.

XX

XX

The invention relates to an antibody produced by a hybridoma selected from the group consisting of AA.FF9 and AA.GE7.3. The antibody is used to stimulate neural and renal cell growth. This sequence corresponds to a nucleic acid sequence of the rat retL1 cDNA of the invention.

XX

SQ Sequence 1878 BP; 389 A; 575 C; 478 G; 436 T; 0 U; 0 Other;

QY

Query Match 96.5%; Score 1867; DB 14; Length 1878;

DB

Best Local Similarity 99.9%; Pred. No. 0;

QY

Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

DB

QY 37 CGCGGCGCCAGCGCAGGCTGTCATCCATCCCGGGGCTCCACCGGCATGGGCT 96

DB

QY 1 CGCGGCGCCAGCGCAGGCTGTCATCCATCCCGGGGCTCCACCGGCATGGGCT 60

QY

QY 97 CTCTTGGAGCCCGCGACCTCCACATGCTGCTACTGCTGCTGCTGCTGCTGCTGCT 156

DB

QY 61 CTCTTGGAGCCCGCGACCTCCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

QY

QY 157 GCCACTTGGAGCAGGAAATCTCCCTTGGCCACAGAGAAAGGTTTGTGAACAGCTGTACCCA 216

DB

QY 121 GCCACTTGGAGCAGGAAATCTCCCTTGGCCACAGAGAAAGGTTTGTGAACAGCTGTACCCA 180

QY

QY 217 GCGCAGAGAAATGCGAGGCTAATCCGCTTGCAGGCTGCGCTACACGACCTGGGCTC 276

DB

QY 181 GCGCAGAGAAATGCGAGGCTAATCCGCTTGCAGGCTGCGCTACACGACCTGGGCTC 240

QY

QY 277 CTGCACTCCAGTTTAAAGCAGGCGCTGCTTAAAGGAGTCTGCAATGCTCTGCAAGCTG 336

DB

QY 241 CTGCACTCCAG - TTAAGCAGGCGCTGCTTAAAGGAGTCTGCAATGCTCTGCAAGCTG 299

QY

QY 337 CCTAGAGCAGCAGAAACAACTCAGGAAACAGCTCTCTGATAGACTGCAAGTGCATTCGCG 396

DB

QY 300 CCTAGAGCAGCAGAAACAACTCAGGAAACAGCTCTCTGATAGACTGCAAGTGCATTCGCG 359

QY

QY 397 CATGAAGCAGCAGCTACCTGTCTGGAATTTATTTAGACCTTACCTCTCCGAGGCT 456

DB

QY 360 CATGAAGCAGCAGCTACCTGTCTGGAATTTATTTAGACCTTACCTCTCCGAGGCT 419

QY

QY 457 TGGTGACTTACAGTTGGATGCTCAACCTATGAAGACACAGTGACCAACCACTCGAA 516

DB

QY 420 TGGTGACTTACAGTTGGATGCTCAACCTATGAAGACACAGTGACCAACCACTCGAA 479

QY

QY 517 AATGAATCTTAGCAAGTTGAACATGCTCAACCAACAGACTCGGACCTCTGCTCAAATTCG 576

DB

QY 480 AATGAATCTTAGCAAGTTGAACATGCTCAACCAACAGACTCGGACCTCTGCTCAAATTCG 539

QY

QY 577 TATGCTGTGACTCTTACAGCAAGTGTGACCGCTTGCAGGCTTACGGGAGGCTATG 636

DB

QY 540 TATGCTGTGACTCTTACAGCAAGTGTGACCGCTTGCAGGCTTACGGGAGGCTATG 599

QY

QY 637 CTCAGGGATCCGCTGCGCAGCGCACTCTGCTTAGCCAGCTGCGCTCTTCTTTAGAA 696

DB

QY 600 CTCAGGGATCCGCTGCGCAGCGCACTCTGCTTAGCCAGCTGCGCTCTTCTTTAGAA 659

QY

QY 657 GCGCAGCAGTCCCAAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 756

DB

QY 660 GCGCAGCAGTCCCAAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719

QY

QY 757 CTGTGGGAGCGCGGCTTAAACATGCGCCCAAGTTGCGCCCTGCTCTGTAACCCC 816

DB

QY 720 CTGTGGGAGCGCGGCTTAAACATGCGCCCAAGTTGCGCCCTGCTCTGTAACCCC 779

QY

QY 817 CAATTGCTGACTCTGCGGAGCTTCTGCGGCGGAGCTTCTGCGGAGCTTCTGCGAGATCAGCTCAT 876

DB

QY 780 CAATTGCTGACTCTGCGGAGCTTCTGCGGCGGAGCTTCTGCGAGATCAGCTCAT 839

QY

QY 877 GGACTTCCAGACCCCACTGCTCATCTTATGGAATCTTGGGAGCTTGTGCACTGAGCAGTC 936

DB

QY 840 GGACTTCCAGACCCCACTGCTCATCTTATGGAATCTTGGGAGCTTGTGCACTGAGCAGTC 899

QY

QY 937 CAGATGTCTGCGGCGATACCTGCGGCTGATTTGGGAGCTGCTGCAATGACCCCAAACTTCATCAG 996

Db 900 CAGATGTCTGGGGCATACCTGGGCTGATTGGGAGTCCATGACCCCAAACTTCATCAG 959  
Qy 997 CAAAGTCAACACTACTGTTCCTTAAGCTGCACCTGCCGAGCGCAGCAACCTACAGGA 1056  
Db 960 CAAAGTCAACACTACTGTTCCTTAAGCTGCACCTGCCGAGCGCAGCAACCTACAGGA 1019  
Qy 1057 CAAAGTGTGAACAGCTGTGAAAGGTCTCTTCCAGAACCCCTGCCCTCGTGGAGGCCATTGCG 1116  
Db 1020 CAAAGTGTGAACAGCTGTGAAAGGTCTCTTCCAGAACCCCTGCCCTCGTGGAGGCCATTGCG 1079  
Qy 1117 AGCTAAGATGCGTTTCCACAGACAGCTCTTCTCCAGAGCTGGGAGACTCTACTTTTTC 1176  
Db 1080 AGCTAAGATGCGTTTCCACAGACAGCTCTTCTCCAGAGCTGGGAGACTCTACTTTTTC 1139  
Qy 1177 AGTGTGCAGCAGCAGACAGCAACCCCTGCTCTGAGACTGCAGCCAGCGCTACCCATTCT 1236  
Db 1140 AGTGTGCAGCAGCAGACAGCAACCCCTGCTCTGAGACTGCAGCCAGCGCTACCCATTCT 1199  
Qy 1237 TTCTTTCTCCATCTTCCCTTTCCTGATTCTGTCGAGACCTCTGTAGCTGGGCTTCTTCAG 1296  
Db 1200 TTCTTTCTCCATCTTCCCTTTCCTGATTCTGTCGAGACCTCTGTAGCTGGGCTTCTTCAG 1259  
Qy 1297 GGTCTCTTTGCTCTCTCCACACACCCAGACTGATTTCAGCGCTGTGGTGGAGAGAACTC 1356  
Db 1260 GGTCTCTTTGCTCTCTCCACACACCCAGACTGATTTCAGCGCTGTGGTGGAGAGAACTC 1319  
Qy 1357 GCCAGCTGTGGAAGACGACGCGTGTACACAGCAACCCGGAACCAACCGGCATTTC 1416  
Db 1320 GCCAGCTGTGGAAGACGACGCGTGTACACAGCAACCCGGAACCAACCGGCATTTC 1379  
Qy 1417 CACAGACATCCCGTCTGCTCCAGAAAGAGTCTTAGAAGTAGGAGCTGTGACCCCTTCGGA 1476  
Db 1380 CACAGACATCCCGTCTGCTCCAGAAAGAGTCTTAGAAGTAGGAGCTGTGACCCCTTCGGA 1439  
Qy 1477 TCCTCAGCGGTAGTTTTCAAACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1536  
Db 1440 TCCTCAGCGGTAGTTTTCAAACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1499  
Qy 1537 CTCCTTAGGACTTTGGGTCAGTTTTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1596  
Db 1500 CTCCTTAGGACTTTGGGTCAGTTTTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559  
Qy 1597 CTCACAGCGCTCTCTCTGTTTCCAGGACACCCAGAGCTAAGGAATCAGTCAATTCCT 1656  
Db 1560 CTCACAGCGCTCTCTCTGTTTCCAGGACACCCAGAGCTAAGGAATCAGTCAATTCCT 1619  
Qy 1657 GTTGCCTTCTCCAGAAAGCAGGCTAAGGGTTCTGAGGTGACTGAGAAAAATGTTTCCTT 1716  
Db 1620 GTTGCCTTCTCCAGAAAGCAGGCTAAGGGTTCTGAGGTGACTGAGAAAAATGTTTCCTT 1679  
Qy 1717 TGTGTGGAAGGTGCTGCTCCAGCTCCAGCTCCCTCTGATGGAAGATTAACCTGCT 1776  
Db 1680 TGTGTGGAAGGTGCTGCTCCAGCTCCAGCTCCCTCTGATGGAAGATTAACCTGCT 1739  
Qy 1777 GGTGTCTTGACTGCTCTGCGAGCAATCTGAACTTTGGGCATGAAGAGCTAAAGTCTT 1836  
Db 1740 GGTGTCTTGACTGCTCTGCGAGCAATCTGAACTTTGGGCATGAAGAGCTAAAGTCTT 1799  
Qy 1837 TGGGTCTTGTAACTCTTACTTGTGCTCCCAAAATCCCTAGTCCCTTGGGTCAAGATT 1896  
Db 1800 TGGGTCTTGTAACTCTTACTTGTGCTCCCAAAATCCCTAGTCCCTTGGGTCAAGATT 1859  
Qy 1897 AAACATTTGACTTAAAA 1915  
Db 1860 AAACATTTGACTTAAAA 1878

RESULT 9  
AD200206  
ID AD200206 standard; cDNA; 1878 BP.  
XX  
AC AD200206;

XX 30-JUN-2005 (first entry)  
DT Mouse Ret ligand 3 (RetL3) partial cDNA, SEQ ID NO:14.  
XX  
DE Cell growth; development; signal transduction; neurological disease;  
XX renal disease; genitourinary disease; neuroprotective; nephrotropic;  
KW cancer; neoplasm; cytotatic; RetL3;  
KW Ret tyrosine kinase receptor ligand 3; Ret ligand 3;  
KW GDNF family receptor alpha 3; GFRA3; ss.  
XX  
OS Mus sp.  
XX  
XX Key Location/Qualifiers  
FH CDS 205..1245  
FT /\*tag= a  
FT /partial  
FT /product= "Mouse RetL3 fragment"  
FT /note= "No start codon given"  
XX  
XX US2005080235-A1.  
XX 14-APR-2005.  
XX  
XX 23-SEP-2003; 2003US-00668936.  
XX  
XX 08-MAY-1996; 96US-0017427P.  
XX 07-JUN-1996; 96US-0019300P.  
XX 16-JUL-1996; 96US-0021859P.  
XX 23-AUG-1996; 96US-0023444P.  
XX 11-APR-1997; 97US-0043533P.  
XX 07-MAY-1997; 97WO-US007726.  
XX 06-NOV-1998; 98US-00187906.  
XX (SANI/) SANICOLA-NADEL M.  
XX (HESS/) HESSON C.  
XX (CATE/) CATE R L.  
XX (WORL/) WORLEY D S.  
XX  
XX Sanicola-Nadel M, Hession C, Cate RL, Worley DS;  
XX  
XX WPI; 2005-305025/31.  
XX P-PSDB; AD200207.  
XX  
XX New polypeptide sequence that interacts with a receptor protein Ret to  
XX trigger dimerization or autophosphorylation, useful in preparing a  
XX composition for treating neurodegenerative disorders, e.g., Alzheimer's  
XX disease.  
XX  
XX Disclosure; SEQ ID NO 14; 67pp; English.  
XX  
XX The invention relates to the murine and human RetL3 (Ret ligand 3)  
XX proteins (AD200209 and AD200213, respectively) and to proteins at least  
XX 80% identical to murine or human RetL3. The invention also discloses  
XX other RetL proteins such as rat RetL1, human RetL1, human RetL2,  
XX fragments of human RetL1, mouse RetL3 and human RetL3, and cDNA sequences  
XX encoding these RetL proteins or protein fragments. Like other RetL  
XX proteins, the RetL3 proteins of the invention interact with the Ret  
XX receptor tyrosine kinase that is encoded by the Ret proto-oncogene.  
XX triggering Ret receptor dimerization or autophosphorylation. The Ret  
XX receptor is expressed during development in a variety of tissues,  
XX including the peripheral and central nervous systems and the kidney. It  
XX is also expressed in some cancers. RetL proteins such as the murine and  
XX human RetL3 proteins, and RetL polynucleotides may be used for  
XX stimulating Ret receptor signaling, thereby promoting renal or neuronal  
XX cell growth or survival and minimizing damage to such tissues after  
XX various insults. They may therefore be used to treat renal disorders  
XX (e.g., renal failure, renal tube defects and renal trauma) or  
XX neurological disorders including neurodegenerative disorders (e.g.,  
XX Alzheimer's disease), bacterial or viral diseases of the nervous system  
XX (e.g., meningitis), neurological damage (e.g. that caused by hemorrhage  
XX or trauma) and developmental neural disorders (e.g., mental retardation).  
XX Conversely, antibodies against RetL may be used to block RetL-Ret



CC receptor signal transduction for inhibiting tumor growth, fusion proteins  
CC -expressing a RetL protein are useful for targeting a drug to Ret receptor  
CC -expressing tumors. Anti-RetL antibodies and RetL fusion proteins may  
CC also be used in medical imaging. The present sequence represents a murine  
CC RetL3 partial cDNA initially identified by a search of an expressed  
CC sequence tag (EST) database using a rat RetL1 peptide sequence, and  
CC isolated from the EST clones AA049894 and AA050083.  
XX  
SQ Sequence 1878 BP; 389 A; 575 C; 478 G; 436 T; 0 U; 0 Other;

Query Match		96.5%; Score 1867; DB 14; Length 1878;
Best Local Similarity		99.9%; Pred. No. 0;
Matches 1878; Conservative		0; Mismatches 0; Indels 1; Gaps 1;
QY	37	CGCGGCGCCAGCGCAGGCGAGCGCTGTCGATCCCGGGCGCTCCACCGCCCATGGGCT 96
DB	1	CGCGGCGCCAGCGCAGGCGAGCGCTGTCGATCCCGGGCGCTCCACCGCCCATGGGCT 60
QY	97	CTCTCGAGCGCGGACCTCCACTGCTGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 156
DB	61	CTCTCGAGCGCGGACCTCCACTGCTGATGATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY	157	GCCACTTGGAGCAGGAACTCCCTTGCACAGGACAGGTTTGTGAACAGCTGTACCCA 216
DB	121	GCCACTTGGAGCAGGAACTCCCTTGCACAGGACAGGTTTGTGAACAGCTGTACCCA 180
QY	217	GCCAGAAAGAAATCGAGGCTAATCCCGCTTGCAGGCTGCTTACAGCAGCTGGGCTC 276
DB	181	GCCAGAAAGAAATCGAGGCTAATCCCGCTTGCAGGCTGCTTACAGCAGCTGGGCTC 240
QY	277	CTGCACCTCAGTTTAAAGCAGGCGCTGCTGCTTGAAGAGTCTGCCATCTCTGCAGACTG 336
DB	241	CTGCACCTCAG-TTAAAGCAGGCGCTGCTGCTTGAAGAGTCTGCCATCTCTGCAGACTG 299
QY	337	CCTAGAGCAGCAGAACACTCAGGAACAGCTCTCTGATAGACTGCAAGTGCATCGGCG 396
DB	300	CCTAGAGCAGCAGAACAACTCAGGAACAGCTCTCTGATAGACTGCAAGTGCATCGGCG 359
QY	397	CATGAAGCAACAGCTTACCTGCTGACATTTATTTGACCGCTTACCCCTGCCCGAAGCT 456
DB	360	CATGAAGCAACAGCTTACCTGCTGACATTTATTTGACCGCTTACCCCTGCCCGAAGCT 419
QY	457	TGGTGACTACGAGTTGGATGTCTCACCTATGAAGACACAGTGAACAGAAACCTTGGAA 516
DB	420	TGGTGACTACGAGTTGGATGTCTCACCTATGAAGACACAGTGAACAGAAACCTTGGAA 479
QY	517	AATGAATCTTAGCAAGTTGAACATGCTGAAACAGAGCTCGGACCTTGCTCAAAATTTGC 576
DB	480	AATGAATCTTAGCAAGTTGAACATGCTGAAACAGAGCTCGGACCTTGCTCAAAATTTGC 539
QY	577	TATGCTGTGTACTCTTTCAGCAAGTGTGACCGCTTGCAGAGGCTTACGGGAGGCATG 636
DB	540	TATGCTGTGTACTCTTTCAGCAAGTGTGACCGCTTGCAGAGGCTTACGGGAGGCATG 599
QY	637	CTCAGGGATCCGCTGCCAGCGCACTCTGCTGCTAGCCAGCTGCGCTCTTTTGGAGAA 696
DB	600	CTCAGGGATCCGCTGCCAGCGCACTCTGCTGCTAGCCAGCTGCGCTCTTTTGGAGAA 659
QY	697	GGCAGCAGAGTCCACGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756
DB	660	GGCAGCAGAGTCCACGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 719
QY	757	CTGTGGGAGCGGCGGCTTAAACCATTCGCCCCAGTTGCGCCCTGCTTCTGTAAACCC 816
DB	720	CTGTGGGAGCGGCGGCTTAAACCATTCGCCCCAGTTGCGCCCTGCTTCTGTAAACCC 779
QY	817	CAATTCCTGGATCTCGGAGCTTCTGCGCTGCGGACCTTTTGTGAGATCAAGCTGAT 876
DB	780	CAATTCCTGGATCTCGGAGCTTCTGCGCTGCGGACCTTTTGTGAGATCAAGCTGAT 839
QY	877	GGACTTCCAGACCCACTGTATGACATCTTGGAGCTTGGAGCTTGGAGCTGAGCAGTC 936
DB	840	GGACTTCCAGACCCACTGTATGACATCTTGGAGCTTGGAGCTTGGAGCTGAGCAGTC 899

RESULT 10  
AAV99331  
ID AAV99331 standard; cDNA; 1699 BP.

QY	937	CAGATGTTCTGCGGCGCATACCTGGGCTGATTTGGAGTCCCATGACCCCAAACTTCATCAG 996
DB	900	CAGATGTTCTGCGGCGCATACCTGGGCTGATTTGGAGTCCCATGACCCCAAACTTCATCAG 959
QY	997	CAAGGTCAACACTACTGTTGCTTAAAGCTGACCTGCGGAGCGAGCGGCACTACAGGA 1056
DB	960	CAAGGTCAACACTACTGTTGCTTAAAGCTGACCTGCGGAGCGAGCGGCACTACAGGA 1019
QY	1057	CGAGTGTGAACAGCTGGAAAGTCTCTTCCAGAACCCCTGCTGCTGCTGCTGCTGCTGCT 1116
DB	1020	CGAGTGTGAACAGCTGGAAAGTCTCTTCCAGAACCCCTGCTGCTGCTGCTGCTGCTGCT 1079
QY	1117	AGCTAAGATGCGTTTCCACAGACAGCTCTTCTCCAGGACTGGGAGACTTACTTTTTC 1176
DB	1080	AGCTAAGATGCGTTTCCACAGACAGCTCTTCTCCAGGACTGGGAGACTTACTTTTTC 1139
QY	1177	AGTGTGTCAGCAGCAGAACCAACCTGCTCTGAGACTGCAAGCCAGGCTTACCCATTC 1236
DB	1140	AGTGTGTCAGCAGCAGAACCAACCTGCTCTGAGACTGCAAGCCAGGCTTACCCATTC 1199
QY	1237	TTCTTTTCTCCATCTCTTCCCTTGAATCTGCTGACACCCCTCTGCTAGCTGGGCTTCTCAG 1296
DB	1200	TTCTTTTCTCCATCTCTTCCCTTGAATCTGCTGACACCCCTCTGCTAGCTGGGCTTCTCAG 1259
QY	1297	GCTCTTGTGCTCTTCCACCAACCCAGACTGATTTGCAAGCTGTGTGGGAGAGAACTC 1356
DB	1260	GCTCTTGTGCTCTTCCACCAACCCAGACTGATTTGCAAGCTGTGTGGGAGAGAACTC 1319
QY	1357	GCCAGCTCTGGAGAGAACGCGAGGCTGTACACAGCAACCCGGAACCAACCCAGGCACTC 1416
DB	1320	GCCAGCTCTGGAGAGAACGCGAGGCTGTACACAGCAACCCGGAACCAACCCAGGCACTC 1379
QY	1417	GCAGACATCCCGTCTGCTCCAGAAAGAGTCTTAGAAGTGAAGGCTGTGACCTTCCGA 1476
DB	1380	GCAGACATCCCGTCTGCTCCAGAAAGAGTCTTAGAAGTGAAGGCTGTGACCTTCCGA 1439
QY	1477	TCTCAGCGGCTAGTTTTCAAACCTTGGCCCTGCTTCTTCTGCTGCTGCTGCTGCTGCT 1536
DB	1440	TCTCAGCGGCTAGTTTTCAAACCTTGGCCCTGCTTCTTCTGCTGCTGCTGCTGCTGCT 1499
QY	1537	CTCCTTAGAGACTTGTGGGTCCAGTTTTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1596
DB	1500	CTCCTTAGAGACTTGTGGGTCCAGTTTTTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
QY	1597	CTCCAGCGCTTCTCTGCTTCCAGAGACCCAGAGGCTAAGGAATCAGTCAATTCCT 1656
DB	1560	CTCCAGCGCTTCTCTGCTTCCAGAGACCCAGAGGCTAAGGAATCAGTCAATTCCT 1619
QY	1657	GTTCCTTCTCCAGGAGCGGCTTAAAGGTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1716
DB	1620	GTTCCTTCTCCAGGAGCGGCTTAAAGGTTCTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1679
QY	1717	TGTGTGAAGGCTGCTGCTCCAGGCTTCCAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1776
DB	1680	TGTGTGAAGGCTGCTGCTCCAGGCTTCCAGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 1739
QY	1777	GCTGTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1836
DB	1740	GCTGTCTTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1799
QY	1837	TGGGCTTGTGTTAACTCTTATCTGCTCCCAAAATTCCTTCCCTAGTCCCTTGGGTCATGAT 1896
DB	1800	TGGGCTTGTGTTAACTCTTATCTGCTCCCAAAATTCCTTCCCTAGTCCCTTGGGTCATGAT 1859
QY	1897	AAACATTTTGAATTTAAAAA 1915
DB	1860	AAACATTTTGAATTTAAAAA 1878

XX AAV99331;  
AC  
XX  
XX 25-MAR-1999 (first entry)  
DE  
XX cDNA encoding a GDNFR-alpha-related protein 3 (GRR3).  
XX  
XX Rat; glial cell-line derived neurotrophic factor receptor; GDNFR;  
KW Glial cell line-derived neurotrophic factor; GDNF; neuroturin;  
KW signal transduction; dopaminergic nerve cell; Parkinson's disease;  
KW Alzheimer's disease; amyotrophic lateral sclerosis;  
KW neurological disorder; diabetes; glaucoma; sensory neuron;  
KW retinal ganglion cell degeneration; sensory neuropathy; retinopathy;  
KW gene therapy; GDNFR-related protein 3; GRR3; ss.  
XX  
XX Rattus sp.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 67..1260  
FT FT /\*tag= a  
FT FT /product= "GRR3"  
XX  
XX WO9854213-A2.  
XX  
XX 03-DEC-1998.  
XX  
XX 27-APR-1998; 98WO-US008486.  
XX  
XX 30-MAY-1997; 97US-00866354.  
XX (AMGE-) AMGEN INC.  
XX  
XX Fox GM, Jing S, Wen D;  
PI  
XX WPI; 1999-080806/07.  
DR P-PSDB; AAW84182.  
XX  
XX New isolated glial cell line-derived neurotrophic factor receptors - used  
PT to develop products for treating e.g. improperly functioning dopaminergic  
PT nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic  
PT lateral sclerosis.  
XX  
XX Disclosure; Fig 17; 318pp; English.  
XX  
XX The present sequence encodes a rat glial cell-line derived neurotrophic  
CC factor receptor (GDNFR)-related protein 3 (GRR3). The protein has similar  
CC functions to GDNFR. GDNFR proteins are functionally characterised by the  
CC ability to bind glial cell line-derived neurotrophic factor (GDNF) and/or  
CC neuroturin specifically, and to act as part of a molecular complex which  
CC mediates or enhances the signal transduction affects of GDNF and/or  
CC neuroturin. The proteins can be used for treating improperly functioning  
CC dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or  
CC amyotrophic lateral sclerosis. They can also be used for treating  
CC neurological disorders associated with diabetes, glaucoma or other  
CC diseases and conditions involving retinal ganglion cell degeneration,  
CC sensory neuropathy caused by injury to, insults to, or degeneration of,  
CC sensory neurons, pathological conditions, or disease or injury-related  
CC retinopathies. The products can also be used for detection, diagnosis,  
CC drug screening and gene therapy  
XX  
SQ Sequence 1699 BP; 341 A; 556 C; 443 G; 359 T; 0 U; 0 Other;

Query Match 67.4%; Score 1304.4; DB 2; Length 1699;  
Best Local Similarity 88.1%; Pred. No. 0;  
Matches 1515; Conservative 0; Mismatches 161; Indels 44; Gaps 7;

QY 28 GGCACGAGCGCGCGCCAGCGCAGGACGCTGTCGATCCGGGCGTCC--ACCC 85  
DB 4 GCGGGTGCACGACGCCGACGACGAGCGCTGCGGGTCCGGCGCTCAGACCC 63  
QY 86 GCCATGGGGCTCTCTGGAGCCGCGACCTCCACTGCTGATGATCTCTGCTACTGTGCTG 145  
DB 64 GCCATGGGGCTCTCTCGGAGCCGCGACCGCGCGCTAGTGTCTCTGCTACTGTGCTG 123

QY 146 TCGTTGTGGCTGCCACTTTGGAGCAGGAAACTCCCTTGGCCACAGAGAAACAGGTTTGTGAAC 205  
DB 124 TCGCTGTGGCTACCCCTTTGGAACAGGAAACTCCCTTCCACAGAGAAACAGGCTTTGTGAAC 183  
QY 206 AGCTGTATCCAGGCGCAGAAAGAAATGCGAGGCTAATCCCGCTTGCAGAGGCTGCCTACCCAG 265  
DB 184 AGCTGTATCCAGGCGCAGAAAGAAATGCGAGGCTAATCCCGCTTGCAGAGGCTGCCTACCCAG 243  
QY 266 CACCTGGGCTCTCTGCACCTTCAGTTTAAAGCAGGCGCTGCCCTTAGAGGAGTCTGCCATG 325  
DB 244 CACCTGGACTCTCTGCACCCCGCAGTCTCAGCAGTCCACTTGCCTTCAGGGGAGTCTGCCACA 303  
QY 326 TCTGCAGACTCCCTAGAGGCGCAGAACAACTCAGGAACAGCTCTCTGATAGACTGCGAGG 385  
DB 304 TCTGCAGGCTGCCCTTGAAGCAGCAGCAACTCAGGAACAGCTCTCTCATAGACTGCGAGG 363  
QY 386 TGCCATCGGCGCATGAAGCACCAAGCTACTGTCTGGACATTTATTTGGACCGTTCAACCT 445  
DB 364 TGCCACCGGCGCATGAAGCACCAAGCTACTGTCTGGACATTTATTTGGACCGTTCAACCT 423  
QY 446 GCCGAGGCTTGGTACTACAGTTGGATGTCTCACCTATGAAGACACAGTGAACGAC 505  
DB 424 GTCCGAAGCCTTGGTACTACAGTTGGACGTCTCACCTATGAAGACACAGTGAACGAC 483  
QY 506 AAACCTTGAAAAATGAATCTTAGCAAGTTTGAACATGCTCAAAACAGACTCCGACCTCTGC 565  
DB 484 AAACCTTGAAAAATGAATCTTAGCAAGTTTGAACATGCTCAAAACAGACTCCGACCTCTGC 543  
QY 566 CTCAAATTTGCTATGCTGTGTACTTTTCAAGCAAGTGTGACCGCTTGCAGAGGCTTAC 625  
DB 544 CTCAAATTTGCTATGCTGTGTACTTTTAAACGAAGTGTGACCGCTTGCAGAGGCTTAC 603  
QY 626 GGGGAGGCTCTCAGGGATCCGCTGCAGCGCACACTCTGCCTTAGCCAGCTGGGCTCC 685  
DB 604 GGGGAGGCTCTCAGGGATCCGCTGCAGCGCACACTCTGCCTTAGCCAGCTGGGCTCC 663  
QY 686 TTCTTTGAAGAGGCGCAGAGTCCACGCTCAGAGTCTGTGCTGTGTCTGCTGTGACCA 745  
DB 664 TTCTTTGAAGAGGCGGCGAGTCCACGCTCAGGGCTGTGCTGTGTCTGCTGTGACCC 723  
QY 746 GAAGATCGGGCTGTGGGGAGCGCGGCTTAACACCATTCGCCCCCGAGTTGGCGCTGCT 805  
DB 724 GAAGATCGGGCTGTGGGGAGCGCGGCTTAACACCATTCGCCCCCGAGTTGGCGCTGCT 783  
QY 806 TCTGTAAACCCCAATTTGCTGTGATCTGCGGAGCTTCTGCGTGTGCGGACCTTTGTGAGA 865  
DB 784 TCTGTGGCCCCCAACTGCTTAGATCTTGGGAGCTTCTGCGGTGTGCGGACCTCTGTGAGA 843  
QY 866 TCAGCCTGTATGGACTTCCAGACCCACTGTCTATCTATGGACATCTCTTGGGACTTGTGCA 925  
DB 844 TCAGCCTGTATGGACTTCCAGACCCACTGTCTATCTATGGACATCTCTTGGGACTTGTGCA 903  
QY 926 ACTGAGCAGTCCAGATGTCTCGGGCAATCTGCGGGCTGTATTTGGGACTTGCATGACCCCA 985  
DB 904 ACTGAGCAGTCCAGATGTCTCGGGCAATCTGCGGGCTTAAATTTGGGACTTGCATGACCCCA 963  
QY 986 AACTTCATCAGCAGGTCAACTACTTGTGCTTGTAGCTGCACTGCGGAGGCGAGCGGC 1045  
DB 964 AACTTCATCAGCAGGTCAACTACTTGTGCTTGTAGCTGCACTGCGGAGGCGAGCGGC 1023  
QY 1046 AACTTCATCAGGACGAGTGTGAACAGCTGGAAGAGTCTTCTCTCCAGAAACCCCTGCTCGTG 1105  
DB 1024 AACTTCATCAGGACGAGTGTGAACAGCTGGAAGAGTCTTCTCTCCAGAAACCCCTGCTCATG 1083  
QY 1106 GAGGCACTTGCAGCTTAAGATCGTTTTCCACAGACAGTCTTTCTCCAGAGACTGGGCGAGAC 1165  
DB 1084 GAGGCCATTGGCGCTAAATGCGTTTCCACAGACAACTCTTCTCCAGGACTGGGCGGAC 1143  
QY 1166 TCTACTTTTTCAGTGTGTGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1225  
DB 1144 TCTACTTTTTCAGTGTGTGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1203

QY 1226 CTACCACTTTCTTTCTCCATCTCCCTTGTATCTGTGACACCTCTGTGTAGCTG 1285  
Db 1204 CTACCCGTTCTGTTCTTTCTTCTATCTCTGCTGTGACACCTCTGTGTAACTG 1263  
QY 1286 GGCCTTCTCAGGCTCTTGTCTCTCCACACACCCAGAGCTGATTTGCAGCCTGTGTG 1345  
Db 1264 GGCCTTCTCAGGCTCTTGTCTCTCCACACACCCAGAGCTGATTTGCAGCCTGTGTG 1323  
QY 1346 GGAGAGAACTCCGCCAGCTGTGGAGAGAGACGACGCTGTACACAGCAACCCGGAACCA 1405  
Db 1324 GGAGAGAAATGCTGGCTCTGGAGAGAGATGCAACACGCTCA----- 1367  
QY 1406 ACCAGGCAATCCGAGACATCCCTGTCTGCTCCAGAGAGTCTT---AGAAGTAGGGC 1462  
Db 1368 -----CTGCACATCTCTGCTCTCAGATGAGTCTTGGAGAGAGCGAGGCG 1414  
QY 1463 TGTGACCTTCG-ATCCGTAGCGGCTAGTTTTCAACTCCCTGCCCCCTCTTCCTTC 1521  
Db 1415 TGTGACCGTTCAGAAATCTGAGCGGCGAGCTTTCAAACTCTCTCTAC-----TTACTC 1467  
QY 1522 TGGCTCAGGCTCTCTCTTAGGACTTTGTGGTCCAGTTTGTCTTCTGTCTGATGG 1581  
Db 1468 CTGCTTGGCTCTCTCTCCAGACCTTGT-ACTCCAGTTTGGCTGTATATTGTGGTGG 1526  
QY 1582 TGATAGGGCTTCACCTCAGCGCTTCTTCTGTTTCCAGACCAACAGAGGCTAAGG 1641  
Db 1527 TGATAGCTTCCACCTCAGCGCTTCTTCTGTTTCCAGACCAACAGG-GGCTAATG 1585  
QY 1642 ATACGATCAATCCCTGTTGCTTCCAGGAGGAGGCTAAGGTTCTGAGGTGACATGA 1701  
Db 1586 ACTCACTCATCTCGTGGTCTCTTCCAGGAGGAGGCTGAGGTTCTGAGGCGAGCTGA 1645  
QY 1702 GAAAAATGTTCTTTGTGTGGAAGCGTGGTCTCCAGCC 1741  
Db 1646 GAAAGATGTTCTTTGTGTGGAAGCGTGGTGTCCAAACC 1685

RESULT 11

AAV99334  
ID AAV99334 standard; cDNA; 1878 BP.  
XX AAV99334;  
XX AC AAV99334;  
XX DT 25-MAR-1999 (first entry)  
XX DE Glial cell line-derived neurotrophic factor receptor gamma 2 cDNA.  
XX KW Glial cell line-derived neurotrophic factor receptor gamma 2;  
KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;  
KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;  
KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;  
KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;  
KW renal disorder; kidney failure; gut dysfunction; regeneration;  
KW cardiomyocyte; epithelium; hepatocyte; db.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 68..1270  
FT /tag= a  
FT /product= "GDNFR-gamma2"  
FT sig\_peptide 68..160  
FT /tag= b  
FT mat\_peptide 161..1267  
FT /tag= c  
XX WO9853069-A2.  
XX PN 26-NOV-1998.  
XX PD 20-MAY-1998; 98WO-US010328.  
XX PF 20-MAY-1997; 97US-0047092P.  
XX PR

PR 27-JUN-1997; 97US-00884638.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PI Ni J, Heu T, Young P, Gentz RL, Ruben SM;  
XX WPI; 1999-070150/06.  
XX P-PSDB; AAW84186.  
XX New isolated glial cell derived neurotrophic factor receptors - used to  
XX develop products for treating e.g. neurodegenerative disorders,  
XX schizophrenia, hypertension, tumours, renal disorders, kidney failure or  
XX gut dysfunction.  
XX Claim 52; Fig 7A-D; 156pp; English.  
XX The present sequence encodes a glial cell line-derived neurotrophic  
XX factor receptor gamma 2 (GDNFR-gamma2). GDNFR-gamma2 shares high homology  
XX with GDNFR-alpha, which is capable of complexing with glial cell line-  
XX derived neurotrophic factor (GDNF) and mediating cell response to GDNF.  
XX The GDNFR polypeptides and agonists can be used for treating disorders  
XX associated with decreased activity of the respective polypeptides. They  
XX can be used for treating neurodegenerative diseases such as amyotrophic  
XX lateral sclerosis, Parkinson's disease, schizophrenia, insomnia, tardive  
XX dyskinesia, hypertension, pituitary adenomas, hyperprolactinemia, thyroid  
XX tumour, renal disorders, kidney failure, gut dysfunction, or for  
XX regeneration of cardiomyocytes, epithelium or hepatocytes. Antagonists of  
XX the polypeptides can be used for treating disorders associated with  
XX increased activity of the respective polypeptides. The products can also  
XX be used for detection, diagnosis and drug screening  
XX Sequence 1878 BP; 391 A; 617 C; 477 G; 393 T; 0 U; 0 Other;  
QY Query Match 49.4%; Score 955.2; DB 2; Length 1878;  
Db Best Local Similarity 73.5%; Pred. No. 8.8e-245;  
Matches 1380; Conservative 0; Mismatches 408; Indels 90; Gaps 9;  
QY 83 CCCGCCATGGGGCTCTCTGTGAGCCCGCGACCTC-----CACTGCTGATGATCTGT 133  
Db 62 CTCGCCATGGTGGCGCCCTTGAACCCGCGACCGCTGCGCCGCTAGTCTGATGTTGCTG 121  
QY 134 CTACTGTGCTGTGTGTGTGCTGCCACTTGGACGAGAACTCCCTTGCACAGAGAAC 193  
Db 122 CTGCTGTGCGCGCGCTGCTGCTCTGCACGCGGAGACCCCTTCCACAGAAAGC 181  
QY 194 AGTTTGTGAACAGCTGTACCCAGCGCAAGAAATGCGAGGCTAATCCCGCTTGCAG 253  
Db 182 CGACTCATGAACAGCTGTCTCCAGGCCAGGAGGAGTGCCAGGCTGATCCCACTGCAGT 241  
QY 254 GCTGCTTACAGCAGCTGTGGGCTCTCTGCACTTCCAGTTTAAGCAGGCGCTGCTTGTAG 313  
Db 242 GCTGCTTACCAACCACTGGATTCTTGCACCTCTAGCATATAAGCACCCTACTGCCCTCAG 301  
QY 314 GAGTCTGCCATGTCTGCAGCTGCTAGGCGCAGACCACTCAGAAACAGCTCTCTG 373  
Db 302 GAGCTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 361  
QY 374 ATAGACTGCAGTGCCATCGGCGCATGAAGCACCAGCTACTGCTGTGCAATTTATTGG 433  
Db 362 ATAGCTGCTATGCTGCGCCAGCGGCGCATGAAGAACCCAGGTGCTGCTGTTGGACATCTATTGG 421  
QY 434 ACCGTTCACTCCCTCCGAAAGCCTTGGTGACTTACAGTTGGATGTCTACCTATGAAGAC 493  
Db 422 ACCGTTCACTCCCTCCGAGCCTTGGTAACTATGAGCTGGATGTCTCTCCCTCTATGAAGAC 481  
QY 494 ACAGTGACCAACCACTTGAAGAAATGAATCTTACAGTTGAACATGCTCAAAACAGAC 553  
Db 482 ACAGTGACCAACCACTTGAAGAAATGAATCTTACAGAACTGAACATGCTCAAAACAGAC 541  
QY 554 TCGGACCTCTGCTCAAAATTTGCTATGCTGTGTACTCTTTCACGAAAGTGTGACCGCTG 613  
Db 542 TCAGACCTCTGCTCAAGTTTGGCATGCTGTGTACTCTCTCATGACAACTGTGACCGGCTG 601



Matches 1357; Conservative 0; Mismatches 404; Indels 90; Gaps 9;

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QY 83 CCGCCATGGGGCTCTCTGAGAGCCCGCACTC-----CACTGCTGATGATCTCTG 133
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 32 CTCGCCATGGTGGCCCTGTAACCGCGACCGCTGCCCGCGTAGTCTCTGATGTGCTG 91
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 CTACTGGTGTGCTGTGTGGCTGCCACTTGGAGCAGGAAACTCCCTTGGCCACAGAGAAC 193
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 92 CTGCTGCTCGCGCGTGGCGCTGCTCTCGAGCGGAGAGCCCTTCCACAGAAAGC 151
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 194 AGGTTGTGAACAGCTGTACACAGGCCAGAAAGAAATGCGAGCTAAATCCCGCTTGCAG 253
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 152 CGACTCATGAACAGCTGTCTTCAGGCCAGAGAAAGTCCAGCTGATCCCACTGCACT 211
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 254 GCTGCTTACAGCACTGCGGCTCTGCACTCTCAGTTTAAAGCAGGCGCTGCGCTTAGAG 313
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 212 GCTGCTTACCACTGATTCCTGCACTCTTAGCATTAAGCAACCCCACTGCGCTCAGAG 271
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 314 GAGTGTGCCATGTCTGCAGACTGCTTAGAGGAGCAGAGAACTCACTCAGGAACAGCTCTG 373
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 272 GAGCCTTCGGTCCCTGCTGACTGCTGAGGAGCAGCAGAACTCAGGAACAGCTCTCTG 331
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 374 ATAGACTGAGTGCATCGGCGCATGAAGCAACCAAGCTACCTGTCTGACATTTATTGG 433
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 332 ATAGGCTGATGTGCCACCGCGCATGAAGAACCAAGTTGCGCTTGGACATCTATTGG 391
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 434 ACGTTTACCTGCCCGAAGCTTGGTGAATGAGTGTCTCAGCTTATGAAGAC 493
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 392 ACGTTTACCTGCCCGAAGCTTGGTGAATGAGTGTCTCAGCTTATGAAGAC 451
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 494 ACAGTGACCAAGCAACCTTGAAGAAATGAACTTTAGCAAGTTGAAATGCTCAAAACAGAC 553
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 452 ACAGTGACCAAGCAACCTTGAAGAAATGAACTTCAAGCAACTGAACTGCTCAAAACAGAC 511
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 554 TGGGACCTTGCTGCTGAAATTTGCTATGCTGTGATCTTCAAGCAAGTGTGACGCTG 613
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 512 TCAGACCTTGCTGCTCAAGTTTGGCATGCTGTGATCTCAATGACAAAGTGTGACGCTG 571
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 614 CGCAGGCTTACGGGAGGATGCTCAGGGATCCGCTGCGAGCGCCACCTCTGCGCTAGCC 673
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 572 CGCAGGCTTACGGGAGGATGCTCAGGGATCCGCTGCGAGCGCCACCTCTGCGCTAGCC 631
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 674 CAGCTGCGCTCTCTTTTGAAGGAGCAGAGTCCACGCTCAGGCTGTGCTGTGTGT 733
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 632 CAGCTGCTCACTTTCTTGAAGGCGCGCGAGCCCAAGCGCAGCGGCTGTCTGTGTC 691
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 734 CCGTGTGACCAAGATCGGGCTGTGGGAGCGCGCGGTAAACCATCGCCCCAGT 793
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 692 CCATGTGCCCCCAACGACCGGGGCTGCGGGGAGCGCGCGCAACACCATCGCCCCAAC 751
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 794 TGGCGCTGCTCTGTAACCCCAATTCCTTGGATCTGCGAGCTTTCGCGTGGGAC 853
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 752 TGGCGCTGCGGCTGTGCGCCCAACTGCTGTGAGCTGCGGCGCTGTCTCTCCGAC 811
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 854 CCTTTGTGAGATCAGCCTGATGGAATTCAGAGCCCACTGTATCTATGACATCTCTT 913
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 812 CCGCTTTGAGATCAGCCTGCTGGATTTCCAGACCCCACTGCCATCCCATGACATCTTA 871
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 914 GGGACTGTGCAACTGAGCAGTCCAGATGTCTGCGGGCATACCTGGGGCTGATGGGACT 973
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 872 GGAATTTGTGCAACAGAGCAGTCCAGATGTCTACGAGCATACCTGGGGCTGATGGGACT 931
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 974 GCATGACCCCAAACTTCAATCAGCAGGTCAACACTACTTGTTCCTTAAGCTGCACTGC 1033
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 932 GCATGACCCCAAACTTGTGAGCAATGTCAACAGATGTTGCCCTTAAGCTGCACTGC 991
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1034 CGAGCAGCGCAACCTACAGCAGTGTGAACAGCTGGAAGGCTCTTCTCCAGAAC 1093
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 992 CGAGCAGTGGCAACCTGAGGAGGAGTGTGAAATGCTGGAAGGCTTCTCTCCACAC 1051
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1094 CCTGCTGCTGAGGAGGCAATGAGCTAAGATGCTTCCACAGACAGCTCTTCTCCAG 1153
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1052 CCTGCTTACAGGAGGCAATGAGCTAAGATGCTTCCACAGCAACTCTTCTCCAG 1111
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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## RESULT 13

AAA88519

ID AAA88519 standard; cDNA; 1829 BP.

XX

AC AAA88519;

XX 22-JAN-2001 (first entry)

XX

XX Human PRO538 cDNA clone DNA48613-1268.

XX

PRO538; human; ocular disease; retinopathy; maculopathy; therapy;  
retinitis pigmentosa; macular degeneration; retinal detachment;  
retinal tear; macular hole; myopia; traumatic choriorretinopathy;  
acute retinal necrosis syndrome; contusion; edema;  
retinal vision occlusion; vascular disease; retinal vasculitis;  
thrombocytopenic purpura; uveitis; retinal occlusion; GFR-alpha-3; ss.

XX Homo sapiens.

XX

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QY 1154 GACTGGGAGACTCTACTTTTTCAGTGTGAGCAGCAGAAACAGCAACCCCTGCTCTGAGA 1213
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1112 GACTGGCCACACCCCTACTCTTGTGATGGCACACAGAAATGAAACCCCTGCTGTGAGG 1171
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1214 CTGCAAGCCAGGCTACCAATCTTTCTTCCATCCCTTCCCTTGAATTCGTGTGACAGC 1273
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1172 CCACAGCCCTGGGTGCGCTCTCTTTTCTCCTGACGCTTCCCTTGAATTCGTCTCTGAGC 1231
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1274 CTCTGTAGCTGGGCTCTCTCAGGCTCTTTTGTCTCTCCACCAACACACAGACTGATTTG 1333
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1232 CTATGGTAGCTGACTTCTCCAGGCGCTCT-TCCCTTCCACCAACACAGGTGACTTTG 1290
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1334 CAGCCTGTGTGGGAGAGAACTCGCCAGCTGTGTGAAGAAGCAGCGTGTCTACACAGC 1393
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1291 CAGGCCACAAGGGGTGAGAAAGGACAGCAGCAGGAAGAGGTGAGTGGCGAGATGAGG 1350
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1394 AACCCGGAACCAACCGGCAATTCGCGACACATCCCGTCTGCTCCAGAGAGGTCTTAGA 1453
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1351 GCACAGG-----AGC 1360
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1454 AGTGAGGCTGTGACCCCTTCCGATCTCAGCGGCTAGTTTCAAACTCCCTTGCCTCTG 1513
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1361 AGCTAAGGTTATGACCTCCAGATCCTTACTGTGTCAGTCTCTATTCCTCCACCCCATC 1420
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1514 CTTCCTTCTGCTCAGGCTGCTCTCTTAGGACTTTTGGGTCCAGTTTTCCTTCTGT 1573
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1421 TCCACTTCTGATTCATGCTGCCCTC-----CTTGGTGGCCACAAATTAGCCATGTCA 1473
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1574 TCTGATGTGATAGCGGCTCACCTC-----AGCGCTTCTCTCTGTTTCCAGGAC 1625
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1474 TCTGCTGTGACCAAGCTCCCAAGCCCTTTCTGAGGCCCTTCTCTTGACTTACAGGAT 1533
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1626 CACCAGAGGCTAAGGAATCAGTCAATCCCTGTTGCCCTC-----TCCAGGGAAG 1674
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1534 CA-CCAGAACTTATAGTTAGCTTCTTATTCATTCAGATTCAGATTAGGTTAGGTTAGG 1592
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1675 GCAGCTAAGGTTCTGAGGTGACTGAGAAATAATTT-TCTTTTGTGGAAAGGCTGTG 1733
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1593 GAGGACTGGGTGTTCTGAGGCGAGCTAGAAAGTCAATCTCTCTTGTGAAGAAGGCTCTCTG 1652
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1734 CTCCAGCTTCCAGCTCCCTCTGATGGAAGATAAACCTGCTGCTGTGCTTGAATGCTCT 1793
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1653 CCCCCCTGCTCC--TCTCTGAGTGGAGGATGGAATACTACTGCTGCACCTGCCCTGTCT 1710
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1794 GCCAGGCAATCTGAACATTTGGGCACTGAAGAGCTAAAGTCTTTGGGTCTTGTTTAACTC 1853
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1711 CCGGATCCTGCGAAACATCTGGGCACTCAGAGCTGAGGCTGTGGGCTTGTCTTATTC 1770
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1854 CTATTACTGTCCCAAAATTCCTTGTGCTGCTTGGGTCAATGATTAACAATTT 1904
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1771 CTATTATTGTCTAAAGTCTCTCTGGGCTCTTGGATCATGATTAACCTTT 1821
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 241 TCCCGCTTGAAGGCTGCTACACGACCTGGGCTCCTGCACCTCCAGTTTAAAGCAGGCC 300
Db 241 TCCCGCTTGAAGGCTGCTACACGACCTGGGCTCCTGCACCTCCAGTTTAAAGCAGGCC 300
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Db 301 GCTGCCCTTAGAGGAGTCTGCCATGTCTGCAGACTGCTCCTAGAGGAGCAGAGCAACTCAG 360
QY 361 GAAAGCTCTCTGATAGACTGAGTGCATCTGGGGGATGAGAGCAACAGCTACCTGTCT 420
Db 361 GAAAGCTCTCTGATAGACTGAGTGCATCTGGGGGATGAGAGCAACAGCTACCTGTCT 420
QY 421 GGACATTTATTGGACCGTTTCACTGCGCCGAGAGCCCTGCTGACTACGAGTTTGGATGCTC 480
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Db 781 CATGCCCGCCAGTTGCGGCTTCTGTAAACCCCAATTCCTGGATCTGCGGAGCTT 840
QY 841 CTGCGTGGGACCTTTGTGAGATCAGCGCTGATGGACTTCCAGACCCACTGTCTATCC 900
Db 841 CTGCGTGGGACCTTTGTGAGATCAGCGCTGATGGACTTCCAGACCCACTGTCTATCC 900
QY 901 TATGACATCTTGGGACTTGTGCAACTGAGCAGTCCAGATGCTGCGGGCATACCTGGG 960
Db 901 TATGACATCTTGGGACTTGTGCAACTGAGCAGTCCAGATGCTGCGGGCATACCTGGG 960
QY 961 GCTGATTTGGGACTGCGGCTTCTATCAGCAAGGTCAACACTACTGTGCGCTT 1020
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QY 1021 AAGCTGCACTTCCGAGGAGCGGCAACCTACAGGACGAGTGTGAACAGCTGGAAAGTTC 1080
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QY 1141 GCTCTTCTCCAGGACTGGGAGACTCTACTTTTTTTCAGTGTGAGCAGCAGAGCAAGCAA 1200
Db 1141 GCTCTTCTCCAGGACTGGGAGACTCTACTTTTTTTCAGTGTGAGCAGCAGAGCAAGCAA 1200
QY 1201 CCCTGCTCTGAGACTGCAAGGAGCTACCCATCTTTCTTCTCCATCTTCCCTTGAT 1260
Db 1201 CCCTGCTCTGAGACTGCAAGGAGCTACCCATCTTTCTTCTCCATCTTCCCTTGAT 1260
QY 1261 TCTGCTGACAGCCCTCTGGTAGCTGGGCTTCTCAGGGTCTTTGCTCTCTCCACACAC 1320
Db 1261 TCTGCTGACAGCCCTCTGGTAGCTGGGCTTCTCAGGGTCTTTGCTCTCTCCACACAC 1320
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QY 1321 CCAGACTGATTTGTCAGGCTGTGTGGGAGAGAACTCGCAGCCTGTGTGAAGAACGCGAG 1380
Db 1321 CCAGACTGATTTGTCAGGCTGTGTGGGAGAGAACTCGCAGCCTGTGTGAAGAACGCGAG 1380
QY 1381 CGTCTACACAGCAACCCGGAACCAACAGGCAATTCGAGCACAATCCGCTCTCTCCAG 1440
Db 1381 CGTCTACACAGCAACCCGGAACCAACAGGCAATTCGAGCACAATCCGCTCTCTCCAG 1440
QY 1441 AAGAGGTCTTAGAAGTGAAGGCTGTGACCCCTTCGATCCTTGAGCGGTAGTTTTCAAACC 1500
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QY 1501 TCCCTTGGCCCTGCTTCTTCTGCTCAGGCTGCTCCTCTTAGGACTTTTGTGGTCCAG 1560
Db 1501 TCCCTTGGCCCTGCTTCTTCTGCTCAGGCTGCTCCTCTTAGGACTTTTGTGGTCCAG 1560
QY 1561 TTTTGGCTTCTGTTCTGATGCTGATAGCGGCTCACCTCAGCGCTTCTTCTGTTTCCC 1620
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Db 1801 AATCTGAACATTTGGGCAATGAAGAGCTTAAAGTCTTTGGGCTTTGTTAACTCTATTAC 1860
QY 1861 TGTCCCCAAATTCCTAGTCCCTTGGGTCAATGATTAACATTTTGACTTTAAAAAAA 1920
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QY 1921 AAAAAAAAAAAAAA 1935
Db 1921 AAAAAAAAAAAAAA 1935
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## RESULT 2

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US-10-668-936-16
; Sequence 16, Application US/10668936
; Publication No. US20050080235A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; and Renal Growth
;
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/668,936
; FILING DATE: 23-Sep-2003
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/187,906
; FILING DATE: 06-NOV-1998
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		APPLICATION NUMBER: PCT/US97/07726	
		FILING DATE: 07-MAY-97	
		APPLICATION NUMBER: US 60/017,427	
		FILING DATE: 08-MAY-96	
		APPLICATION NUMBER: US 60/019,300	
		FILING DATE: 07-JUN-96	
		APPLICATION NUMBER: US 60/021,859	
		FILING DATE: 16-JUL-96	
		APPLICATION NUMBER: US 60/043,533	
		FILING DATE: 10-APR-97	
		ATTORNEY/AGENT INFORMATION:	
		NAME: Kaplan, Warren A.	
		REGISTRATION NUMBER: 34,199	
		REFERENCE/DOCKET NUMBER: A008 PCT CIP	
		TELECOMMUNICATION INFORMATION:	
		TELEPHONE: 617-679-2400	
		TELEFAX: 617-679-2838	
		INFORMATION FOR SEQ ID NO: 16:	
		SEQUENCE CHARACTERISTICS:	
		LENGTH: 1889 base pairs	
		TYPE: nucleic acid	
		STRANDEDNESS: single	
		TOPOLOGY: linear	
		MOLECULE TYPE: cDNA	
		FEATURE:	
		NAME/KEY: CDS	
		LOCATION: 41..1231	
		SEQUENCE DESCRIPTION: SEQ ID NO: 16:	
		US-10-668-936-16	
		Query Match 97.5%; Score 1887; DB 9; Length 1889;	
		Best Local Similarity 100.0%; Pred. No. 0;	
		Matches 1887; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	49	CGCAGCGAGCGCTGCGCATCCCGGGGTCCACCGCCATGGGGCTCTCTCGAGCCC	108
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QY	109	GGGACCTCCACCTGCTGATGATCCTCTACTGTGTGCTGTGTGGCTGCCACTTGGAGC	168
DB	61	GGGACCTCCACCTGCTGATGATCCTCTACTGTGTGCTGTGTGGCTGCCACTTGGAGC	120
QY	169	AGGAACTCCCTTGGCCACAGAGAAACAGGTTTGTGAACAGCTGTACCCAGGGCCAGAA	228
DB	121	AGGAACTCCCTTGGCCACAGAGAAACAGGTTTGTGAACAGCTGTACCCAGGGCCAGAA	180
QY	229	ATGCGAGGCTATCCGGCTTGAAGCTGCTTACAGCACTGGGCTCTCTGCACTCCAG	288
DB	181	ATGCGAGGCTATCCGGCTTGAAGCTGCTTACAGCACTGGGCTCTCTGCACTCCAG	240
QY	289	TTTAAGCAGCGCGCTGCCCTTAGAGAGTCTGCCATGTCTGAGACTGCTAGAGGAGC	348
DB	241	TTTAAGCAGCGCGCTGCCCTTAGAGAGTCTGCCATGTCTGAGACTGCTAGAGGAGC	300
QY	349	AGAACTCAGGAAACAGCTCTCTGATAGACTGCGAGGTGCCATCGGCGCATGAAGCA	408
DB	301	AGAACTCAGGAAACAGCTCTCTGATAGACTGCGAGGTGCCATCGGCGCATGAAGCA	360
QY	409	AGCTACCTGCTGGACATTTATGGACCGTTTACCCCTGCCGAGCCCTTGGTACTAGA	468
DB	361	AGCTACCTGCTGGACATTTATGGACCGTTTACCCCTGCCGAGCCCTTGGTACTAGA	420
QY	469	GTGTGATGTCTCACCTATGAAGACACAGTGTACCCAGCAACCTCGGAAATGAATCTT	528
DB	421	GTGTGATGTCTCACCTATGAAGACACAGTGTACCCAGCAACCTCGGAAATGAATCTT	480
QY	529	CAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCTCAAAATTTGCTGTGTAC	588
DB	481	CAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCTCAAAATTTGCTGTGTAC	540
QY	589	TCTTACGACAGTGTACCGCTTGGCAGGCTTACGGGAGGATGCTCAGGGATCGG	648
DB	541	TCTTACGACAGTGTACCGCTTGGCAGGCTTACGGGAGGATGCTCAGGGATCGG	600

QY	649	CTGCCAGCGCCACTCTGCTAGCCAGCTGCGCTCTCTTTTGAAGGAGCAGAGTC	708
DB	601	CTGCCAGCGCCACTCTGCTAGCCAGCTGCGCTCTCTTTTGAAGGAGCAGAGTC	660
QY	709	CCAGCTCAGGGTCTGCTGCTGCTGTCCTGTCACCAAGAGATCGGGCTGCGGGAGCG	768
DB	661	CCAGCTCAGGGTCTGCTGCTGCTGTCCTGTCACCAAGAGATCGGGCTGCGGGAGCG	720
QY	769	CGCGGTAAACACCATCGCCCGCTGCGCTTCTGTAAACCCCAATTGCTGGA	828
DB	721	CGCGGTAAACACCATCGCCCGCTGCGCTTCTGTAAACCCCAATTGCTGGA	780
QY	829	TCTCGGAGCTTCTGCGGTGCGGACCTTTGTGAGATCAGCCTGATGAGATTCACAG	888
DB	781	TCTCGGAGCTTCTGCGGTGCGGACCTTTGTGAGATCAGCCTGATGAGATTCACAG	840
QY	889	CCACTGTATCCTATGACATCTTGGGACTTGTGACCTGAGCACTGAGATGCTGCG	948
DB	841	CCACTGTATCCTATGACATCTTGGGACTTGTGACCTGAGCACTGAGATGCTGCG	900
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DB	901	GGCATACCTGGGGCTGATTTGGGACTGCGCATGACCCCAAACTTCATCAGCAAGGTCAAC	960
QY	1009	TACTGTGCTTAAAGCTGACCTGCGGAGGCGGCGCAACCTACAGGACGATGTGAACA	1068
DB	961	TACTGTGCTTAAAGCTGACCTGCGGAGGCGGCGCAACCTACAGGACGATGTGAACA	1020
QY	1069	GCTGGAAAGGTCTTCTCCAGAAACCTGCTGCTGGAGGCCATTGAGCTTAAGATCGG	1128
DB	1021	GCTGGAAAGGTCTTCTCCAGAAACCTGCTGCTGGAGGCCATTGAGCTTAAGATCGG	1080
QY	1129	TTTCCACAGACAGCTCTTCTCCAGGACTGGGAGACTCTACTTTTTCAGTGGTGCAGCA	1188
DB	1081	TTTCCACAGACAGCTCTTCTCCAGGACTGGGAGACTCTACTTTTTCAGTGGTGCAGCA	1140
QY	1189	GCAGAACAGCAACCTGCTGTGAGACTGAGCCAGGCTACCCATTTCTTTCTTCTCAT	1248
DB	1141	GCAGAACAGCAACCTGCTGTGAGACTGAGCCAGGCTACCCATTTCTTTCTTCTCAT	1200
QY	1249	CTTTCCCTTGAATCTGCTGACAGCCCTGCTGCTGAGCTGCTGAGGCTCTTGTGTC	1308
DB	1201	CTTTCCCTTGAATCTGCTGACAGCCCTGCTGCTGAGCTGCTGAGGCTCTTGTGTC	1260
QY	1309	TCTCCACACACCCAGACTGATTTGCACTGCTGCTGGGAGAGAACTCCGAGGCTGTGG	1368
DB	1261	TCTCCACACACCCAGACTGATTTGCACTGCTGCTGGGAGAGAACTCCGAGGCTGTGG	1320
QY	1369	AAGAAGACGAGCTGTGTACACAGCAACCCGGAACCAACAGGCAATTCGCGAGCAATCC	1428
DB	1321	AAGAAGACGAGCTGTGTACACAGCAACCCGGAACCAACAGGCAATTCGCGAGCAATCC	1380
QY	1429	CGTCTGCTCCAGAGAGGCTTTAGAAGTGAAGGCTGTGACCCCTTCCGATCTGAGCGCT	1488
DB	1381	CGTCTGCTCCAGAGAGGCTTTAGAAGTGAAGGCTGTGACCCCTTCCGATCTGAGCGCT	1440
QY	1489	AGTTTTCAAAACCTCCCTTGGCCCTGCTTCTTCTGCTGCTGAGGCTGCTCTCTTAGGACT	1548
DB	1441	AGTTTTCAAAACCTCCCTTGGCCCTGCTTCTTCTGCTGCTGAGGCTGCTCTCTTAGGACT	1500
QY	1549	TTGTGGGTCCAGTTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1608
DB	1501	TTGTGGGTCCAGTTTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1560
QY	1609	TTCTGTTTCCAGGACCAACCCAGAGGCTAAGGATCAGTCAATCCCTGTTGCTTCTTCC	1668
DB	1561	TTCTGTTTCCAGGACCAACCCAGAGGCTAAGGATCAGTCAATCCCTGTTGCTTCTTCC	1620
QY	1669	AGGAGGCGAGGCTTAAGGGTCTGAGGCTGACGTGAGAAAATGTTTCTTTTGTGGAAGGC	1728
DB	1621	AGGAGGCGAGGCTTAAGGGTCTGAGGCTGACGTGAGAAAATGTTTCTTTTGTGGAAGGC	1680

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QY 1789 GCTCTGCCAGGCAATCCTGAAACATTTGGGCATGAAGAGCTAAAGTCTTTGGTCTTTGTTT 1848  
Db 1741 GCTCTGCCAGGCAATCCTGAAACATTTGGGCATGAAGAGCTAAAGTCTTTGGTCTTTGTTT 1800  
QY 1849 AACTCTATTACTGTCCTCCCAATTCCTCTAGTCCCTTGGGTGATGATTAACATTTTGAC 1908  
Db 1801 AACTCTATTACTGTCCTCCCAATTCCTCTAGTCCCTTGGGTGATGATTAACATTTTGAC 1860  
QY 1909 TTAATAAAAAAAAAAAAAAAAAAAAAA 1935  
Db 1861 TTAATAAAAAAAAAAAAAAAAAAAAAA 1887

RESULT 3  
US-10-668-936-14  
; Sequence 14, Application US/10668936  
; Publication No. US20050080235A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural  
; and Renal Growth  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS: 21  
; ADDRESSEE: Biogen, Inc.  
; STREET: 14 Cambridge Center  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02142

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/10/668,936  
; FILING DATE: 23-Sep-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/187,906  
; FILING DATE: 06-NOV-1998  
; APPLICATION NUMBER: PCT/US97/07726  
; FILING DATE: 07-MAY-97  
; APPLICATION NUMBER: US 60/017,427  
; FILING DATE: 08-MAY-96  
; APPLICATION NUMBER: US 60/019,300  
; FILING DATE: 07-JUN-96  
; APPLICATION NUMBER: US 60/021,859  
; FILING DATE: 16-JUL-96  
; APPLICATION NUMBER: US 60/043,533  
; FILING DATE: 10-APR-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kaplan, Warren A.  
; REGISTRATION NUMBER: 34,199  
; REFERENCE/DOCKET NUMBER: A008 PCT CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-679-2400  
; TELEFAX: 617-679-2838

INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1878 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 205..1242  
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-10-668-936-14  
Query Match 96.5%; Score 1867; DB 9; Length 1878;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1878; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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Db 1 CGCGCGCGCCAGCCAGCAGAGCGCTGTGCATCCCGGGCGTCCACCCGCCATGGGGCT 60  
QY 97 CTCTGGAGCCCGGAGACCTCCACTGTGTGATGATCTCTGTCTACTGTGTCTGTGTGGCT 156  
Db 61 CTCTGGAGCCCGGAGACCTCCACTGTGTGATGATCTCTGTCTACTGTGTCTGTGTGGCT 120  
QY 157 GCCACTTTGGAGCAGGAACTCCCTTGGCCACAGAGAAACAGGTTTGTGAACAGCTGTACC 216  
Db 121 GCCACTTTGGAGCAGGAACTCCCTTGGCCACAGAGAAACAGGTTTGTGAACAGCTGTACC 180  
QY 217 GCCAGAAAGAAATGCGAGGCTAATCCCGCTTGTCAAGGCTGCCCTACCAGCACCTGGGCTC 276  
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QY 337 CCTAGAGCAGCAGAAACAACTCAGAAACAGCTCTCTGATAGACTGCAGTGCATCGCGG 396  
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Db 724 GAAGATCGGGCTGTGGGAGCGCGCGCAACACCATCGCCCCAGTTGGCCCTCCG 783
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Db 784 TCTGTGGCCCCCAATGCTAGATCTTGGAGCTTCTCGGCTGGGACCCCTCTGTGAGA 843
Qy 866 TCACGCTGATGGACTTCAGACCCACTGTCTATATGACATCTTGGGACTTGTGA 925
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Qy 926 ACTGAGCAGTCCAGATGTCTGGGCACTACCTGGGCTGATTTGGGACTGCCATGACCCCA 985
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Qy 1642 AATCAGTCAATTCCTGTTGCTTCTCCAGGAGGCGAGGCTAAGGGTCTGAGGTGACTGA 1701
Db 1586 ACTCACTCAATTCCTGTTGCTTCTCCAGGAGGCGAGGCTGAGGGTCTGAGGAGCTGA 1645
Qy 1702 GAAATAATGTTCTTGTGTGGAAGGCTGGTGTCTCCAGCC 1741
Db 1646 GAAAGATGGTCCCTTTGTGAGGAGGCTGGTGGTCCAAACC 1685
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## RESULT 5

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US-09-828-366-15
; Sequence 15, Application US/09828366
; Patent No. US20020010137A1
; GENERAL INFORMATION:
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; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klein, Robert D.
; APPLICANT: Napier, Mary
; APPLICANT: Wood, William I.
; APPLICANT: Yuan, Jean
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
; FILE OF INVENTION: CELL GROWTH
; FILE REFERENCE: P1694R1C1
; CURRENT APPLICATION NUMBER: US/09/828,366
; PRIOR FILING DATE: 2001-04-05
; Prior filing data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 15
; LENGTH: 1829
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-828-366-15
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Query Match 48.3%; Score 934.6; DB 3; Length 1829;
Best Local Similarity 73.3%; Pred. No. 2.6e-272;
Matches 1357; Conservative 0; Mismatches 404; Indels 90; Gaps 9;
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Qy 83 CCGCCATGGGCTCTCTCGAGCGCGGACCTC-----CACTGCTGATGATCTG 133
Db 32 CTCGCCATGGTGCCTCCCTGAAACCCGCGACCGTGCCTGCTGCTGCTGCTG 91
Qy 134 CTACTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 193
Db 92 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 151
Qy 194 AGGTTTGTGAACAGCTGTACCCAGGCCAGAAAGAAATGCGAGGCTAATCCCGCTTGAAG 253
Db 152 CGACTCATGAACAGCTGTCTCAGGCCAGGAGGAAGTGCAGGCTGATCCACCTGCAGT 211
Qy 254 GCTGCTTACAGCAGCTGGGCTCTGCACTTCCAGTTTAAAGCAGCGCTGCTGCTGAG 313
Db 212 GCTGCTTACAGCAGCTGGGCTCTGCACTTCCAGTTTAAAGCAGCGCTGCTGCTGAG 271
Qy 314 GAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 373
Db 272 GAGCTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 331
Qy 374 ATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 433
Db 332 ATAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 391
Qy 434 ACCGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 493
Db 392 ACCGTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 451
Qy 494 ACAGTGAACAGCAAAACCTGGAATAATGAAATTTAGCAAGTTGAAACATGCTCAAAACAGAC 553
Db 452 ACAGTGAACAGCAAAACCTGGAATAATGAAATTTAGCAAGTTGAAACATGCTCAAAACAGAC 511
Qy 554 TCGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
Db 512 TCAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 571
Qy 614 CGCAAGGCTTACGGGAGGCTGCTGAGGATCCGCTGCGAGCGCCAGCTGCTGCTGCTGCTG 673
Db 572 CGCAAGGCTTACGGGAGGCTGCTGAGGATCCGCTGCGAGCGCCAGCTGCTGCTGCTGCTG 631
Qy 674 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733
Db 632 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 691
Qy 734 CCCTGTGCAACAGAGATGCGGGCTGTGGGAGGCGGCGGTGAACATCGCCCCCAGT 793
Db 692 CCATGTGCCCCCAACGACCGGGGCTGCGGGAGCGCGCGGCGCAACATCGCCCCCAGT 751
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Qy	434	ACCGTTCA	CCCTGCGG	AGAGCCTT	GGTGACTA	CGAGTTGG	ATGTCCT	CACCCCTATGA	AGAC	433
Db	557	ACCGTTCA	CCGTCGCG	CAGCCTT	GGTAACTAT	GAGCTGG	ATGTCT	CCCCCTATGA	AGAC	616
Qy	494	ACAGTGAC	CAGCAAC	CCCTGMAA	TCATTTAG	CAAGTTGA	ACATGCT	CAACACGAC	553	
Db	617	ACAGTGAC	CAGCAAC	CCCTGMAA	TCATTTAG	CAACACTGA	ACATGCT	CAACACGAC	676	
Qy	554	TCGGACCT	CTGCCTCA	AAATTTGCT	GTATGCTGT	GTACTCTT	CACGAC	AAAGTGTGAC	CGCCTG	613
Db	677	TCAGACCT	CTGCCTCA	AGTTTGC	ATGCTGTGT	TACTCTCA	ATGAC	AGTGTGAC	CGGCTG	736
Qy	614	CGCAAGGC	CTACGGGG	AGGCATG	CTAGGATTC	CGCTGCC	AGCGCC	CACTCTTGC	CTAGCC	673
Db	737	CGCAAGGC	CTACGGGG	AGGCATG	CTCGGG	CCCCACTGCC	CAGCGCCA	CGTCTGC	CTCAGG	796
Qy	674	CAGCTGCG	CTCTTTTG	AGAGG	CAGCAGAG	TCACAG	CTCCACG	CTCAGGG	CTGCTGTGTGT	733
Db	797	CAGCTGCT	CACTTTCT	TGAGAG	CGCCCG	AGCCCC	CAGCGC	AGG	CCCTGTACTGTGTC	856
Qy	734	CCCTGTGC	ACCAGAA	TGCGGG	CTGTGGGG	AGCGGG	CGGTAA	CCATCG	CCCCCCCAGT	793
Db	857	CCATGTGC	CCCCCA	ACGACCG	GGGCTCGGG	GAGCGCG	CGCAAC	CCATCG	CGCCCCCAAC	916
Qy	794	TGCGCCCT	CGCTTCTGT	AAACCC	CCAAATG	CGCTG	ATCTGCG	AGCTTCTG	CGCTGCGG	853
Db	917	TGCGCGCT	CGCGCTGT	GGCCCC	CAACTG	CGCTG	AGCTGCG	GGCGCTCT	CTCTTCTCCGAC	976
Qy	854	CTTTGTGC	AGATCAC	CGCTGTAG	TGCACTT	CCAGAC	CCACTGT	CATCTAT	TGACATCCTT	913
Db	977	CCGCTTTG	CGAGATCA	CGCTTGT	TGATTTT	CGAGAC	CCACTGT	CCATCTAT	TGACATCCTT	1036
Qy	914	GGGACTTT	GTGCAACT	GTAGC	AGTCCAG	ATGTCTG	CGGCGCAT	CCCTGG	GGCGCTGATTTGGG	973
Db	1037	GGAACTTT	GTGCAAC	CAGAG	CGAGTCC	CAGATGCT	ACGAG	CACTAC	CTGGGGCTGATTTGGG	1096
Qy	974	GCCATG	ACCCCA	ACTTCAT	CAGCA	AGGTCA	ACTACTG	TGCTTAA	CGCTGCACTGC	1033
Db	1097	GCCATG	ACCCCA	ACTTTTG	CAGCA	CAATGTCA	ACACCA	AGTGTG	CTTTAA	1156
Qy	1034	CGAGG	CAGCGC	CACTAC	AGGACG	AGTGTGA	CAGCTG	GAAAG	GTCTCTTCC	1093
Db	1157	CGAGG	CAGTGG	CAACCTG	CAGGAG	AGTGTGA	ATGCTG	GAAGG	TTCTTCTCC	1216
Qy	1094	CCCTG	CCCTGTG	AGGCAAT	TGCAG	CTAAAGAT	TGCGTTT	CCACAG	ACAGCTCTTCTCC	1153
Db	1217	CCCTG	CCCTCAG	GGAGCC	ATG	CAGCTA	AGATG	GGTTTT	CACAGC	1276
Qy	1154	GACTGG	GCAGACT	CTATTTTT	TTCA	GTGGTGC	GCAGC	AGAAC	CCCTGCTGTG	1213
Db	1277	GACTGG	GCACAC	CCCTACT	TTTGTG	TGATG	GCACAC	CAAGAA	ACCCCTGCTGTG	1336
Qy	1214	CTGCAG	CGCCAGG	CTAC	CCCATTTCTTT	CTTCC	ATCTCC	CTTGGAT	TCGTGCG	1273
Db	1337	CCACAG	CCCTGG	GGGCCCT	CTCTTTT	CTCTG	CAGCTT	CCCTTGA	TTCTGCTC	1396
Qy	1274	CTCTGT	AGCTGG	GGCTTCT	CTCAG	GGTCTTT	GTCTCT	CCACCA	CCACAG	1333
Db	1397	CTATGT	AGTGTG	AGCTTT	CCCC	CAGG	CCCTCT	TC	CCCTC	1455
Qy	1334	CAGCCT	GTGTGG	GAGAACT	CGCAG	CCCTGTG	GAAGA	AGACG	ACGCTGTAC	1393
Db	1456	CAGCCC	CA	AGGGGTG	AGGAAAG	CAGCAG	CAGAGG	AGGAGT	GCAGTGG	1515
Qy	1394	AACCCG	GAA	CC	AACCG	CA	ATCC	CGTCTG	CTCCAG	1453
Db	1516	GCA	CAGG	-----	-----	-----	-----	-----	-----	1525
Qy	1454	AGTCAG	GGCTGTG	ACCTT	CCGAT	CTCCTG	AGCGGCTAG	TTTTT	CAAA	1513
Db	1526	AGCTA	AGGGTTAT	GA	ACCTC	AGATCC	CTTAT	CTG	GTCTC	1585
Qy	1514	CTTCTCT	TTG	GGCTCAG	GGCTG	CTCTCT	CTTAGG	ACTTTGT	GGGTCCAG	1573

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Db      1586   TCCACTTCTGATTCAGTGCTGCCCTC-----CTTGGTGGCCACAATTTAGCCAATGTCA 1638
Qy      1574   TCTGATGGTGATTAGCGGCTCACCTCC-----AGCGCTTCTTCTCTGTTTCCCCAGGAC 1625
Db      1639   TCTGGTGGTGACAGCTCCACCAAGCCCCTTTGTGAGGCCCTTCTCTTGTACTACCAGGAT 1698
Qy      1626   CACCAGAGGCTAAGGAATCAGTCATTCCTCTGTTCCTTC-----TCCAGGAAG 1674
Db      1699   CA-CCAGAATCTAATAAGTTAGGCTTTCTCTATTGCAATCCAGATTAGGGTTAGGGTAGG 1757
Qy      1675   GCAGGCTAAGGTTCTGAGGTGACTGAGAAAATGTT-TCCTTTGTGTGGAAGGCTGGTG 1733
Db      1758   GAGGACTGGGTGTTCTGAGGCAGCCTAGAAAGTCATTCTCTTTGTGAAGAAGGCTCCTG 1817
Qy      1734   CTCGAGGCTCCAGGCTCCCTCTCGAATGGAAGATAAAAAACCTGCTGGTGTCTTTGACTGCTCT 1793
Db      1818   CCCCTCGTCTCC--TCCTCTGAGTGGAGATGGAAGAACTACTGCCTGCACTGCCCTGTC 1875
Qy      1794   GCCAGGCAATCTCGAACATTTGGGCGCATGAAGAGCTAAAGTCTTTGGGTCTGTGTTTAATC 1853
Db      1876   CCQGATCTCTGCCGAACATCTGGGCGCATCAGGAGCTGGAGGCTGTGGGCGCTTGTCTTATTC 1935
Qy      1854   CTATTACTGTCCCAAAATTCCTCCCTAGTCCTCTGCTGCTGCTCATCATTAACAATTT 1904
Db      1936   CTATTATGTCTAAAGTCTCTCTGGGCTCTTGATCATGATTAACCTTT 1986

RESULT 8
US-10-668-936-20
; Sequence 20, Application US/10668936
; Publication No. US20050080235al
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural
; ; ;
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/668,936
; FILING DATE: 23-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/187,906
; FILING DATE: 06-NOV-1998
; APPLICATION NUMBER: PCT/US97/07726
; FILING DATE: 07-MAY-97
; APPLICATION NUMBER: US 60/017,427
; FILING DATE: 08-MAY-96
; APPLICATION NUMBER: US 60/019,300
; FILING DATE: 07-JUN-96
; APPLICATION NUMBER: US 60/021,859
; FILING DATE: 16-JUL-96
; APPLICATION NUMBER: US 60/043,533
; FILING DATE: 10-APR-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A008 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-679-2400
; TELEFAX: 617-679-2838
;

```





Db 808 ACCCACTGCCATCCCATGACATCTAGGAATCTGTGCAACAGAGCAGTCCAGATGTCTA 867  
Qy 947 CGGGCATACCTGGGGCTGATTTGGGAGTCCCATGACCCCAAACTTCATCAGCAAGTCAAC 1006  
Db 868 CGAGCATACCTGGGGCTGATTTGGGAGTCCCATGACCCCAAACTTTGTGAGCAATGTCAAC 927  
Qy 1007 ACTACTGTTGCTTAAAGCTGCACCTGCCGAGGACGCGGCAACCTACAGGACGAGTGTCAA 1066  
Db 928 ACCAGTGTGCTTAAAGCTGCACCTGCCGAGGACGCGGCAACCTTCAGGAGGAGTGTCAA 987  
Qy 1067 CAGCTGGAAGGTCTTTCTCCAGAACCCCTGCTGCTGGAGGCGCAATTCAGAGCTAAGATG 1126  
Db 988 ATGCTGGAAGGTCTTTCTCCCAACCCCTGCTCAGCGAGGCGCAATTCAGAGCTAAGATG 1047  
Qy 1127 GCTTTCCACAGACAGCTCTTCTCCAGACCTGGGACAGACTCTACTTTTTCAGTGTGTGCGAG 1186  
Db 1048 GCTTTTCCACAGCAACTCTTCTCCAGACCTGGGACAGACTCTACTTTTTCAGTGTGTGCGAG 1107  
Qy 1187 CAGCAGAACAGCAACCCCTGCTGAGACTGCAGGCCAGGCTACCCCAATTCCTTTCTTCCTCC 1246  
Db 1108 CACAGATGAACCCCTGCTGTGAGGCCACAGCCCTGGGTGCCCTCTCTTTTCTCCTGCG 1167  
Qy 1247 ATCTTCCCTGATTCCTGCTGAGACCTCTCTGGTAG 1282  
Db 1168 ACGCTTCCCTGATTCGCTCTGAGCCTATGGTAG 1203

RESULT 11

US-10-668-936-18  
; Sequence 18, Application US/10668936  
; Publication No. US20050080235A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural  
; and Renal Growth  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Biogen, Inc.  
; STREET: 14 Cambridge Center  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02142  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/668,936  
; FILING DATE: 23-Sep-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/187,906  
; FILING DATE: 06-NOV-1998  
; APPLICATION NUMBER: PCT/US97/07726  
; FILING DATE: 07-MAY-97  
; APPLICATION NUMBER: US 60/017,427  
; FILING DATE: 08-MAY-96  
; APPLICATION NUMBER: US 60/019,300  
; FILING DATE: 07-JUN-96  
; APPLICATION NUMBER: US 60/021,859  
; FILING DATE: 16-JUL-96  
; APPLICATION NUMBER: US 60/043,533  
; FILING DATE: 10-APR-97  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kaplan, Warren A.  
; REGISTRATION NUMBER: 34,199  
; REFERENCE/DOCKET NUMBER: A008 PCT CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-679-2400  
; TELEFAX: 617-679-2838  
; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1271 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 2..946  
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-668-936-18  
  
Query Match 38.8%; Score 751.6; DB 9; Length 1271;  
Best Local Similarity 82.5%; Pred. No. 8e-217;  
Matches 873; Conservative 0; Mismatches 184; Indels 1; Gaps 1;  
  
Qy 344 GCAGCAGAACACTCAGGAACAGCTCTCTGATAGACTGCGAGTGCATCGCGCATGAAG 403  
Db 11 GAAACACCTCAACTCAGGAACAGCTCTCTGATAGGCTGCTATGTCACCGCGCATGAAG 70  
Qy 404 CACCAAGCTACCTGCTGCGACATTTATTGGACCGTTTCCACCTGCCGGAAGCCTTGTGTAC 463  
Db 71 AACAGGTGCTGCTGCGACATCTATGGACCGTTTCCACCTGCCGAGCCTTGTGTAAAC 130  
Qy 464 TACAGTTGGATGCTCACCCTATGAAGACACAGTGCACGAAACCCCTGGAAATGAAT 523  
Db 131 TATGAGCTGGATGCTCCCTCTATGAAGACACAGTGCACGAAACCCCTGGAAATGAAT 190  
Qy 524 CTTAGCAAGTTGAACATGCTCAAAACAGACTCGGACCTCTGCTCAAAATTTGCTATGCTG 583  
Db 191 CTCAGCAAACTGAACATGCTCAAAACAGACTCGAGACCTCTGCTCTCAAGTTTGGCCATGCT 250  
Qy 584 TGTACTCTTACGACAAAGTGTGACCGCTCGCGAAGGCTTACGCGGAGGCAATGCTCAGGG 643  
Db 251 TGTACTCTCAATGACAAAGTGTGACCGCTCGCGAAGGCTTACGCGGAGGCTGCTCCGG 310  
Qy 644 ATCCGCTGCCAGCGCCACCTCTGCTAGCCAGCTGCGCTCTCTTTTGAAGAGCGCAGCA 703  
Db 311 CCCCACTGCCAGCGCCACCTCTGCTCAGGAGCTGCTCACTTTTTCGAGAGGCGCGCC 370  
Qy 704 GAGTCCCAAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763  
Db 371 GAGCCCCACGCGCAGGCGCTGCTACTGTGCCCATGCTGCCCAACGACCGGGGCTCGGG 430  
Qy 764 GAGCGCGGCTTAACACCATCGCCCGCTTGGCGCTTCTGTAAACCCCAATGTC 823  
Db 431 GAGCGCGGCGCAACACCATCGCCCGCTTGGCGCTTCTGTGCGCTGCTGCGCTGCTGCGCTG 490  
Qy 824 CTGGATCTGCGGAGCTTCTGCGCTGCGGACCTTTTGTGCGAGATCACGCTGATGAGACTTC 883  
Db 491 CTGGAGCTGCGGCGCTTCTGCTTCTCGACCGCTTTTGCAGATCACGCTGCTGCTGATTTTC 550  
Qy 884 CAGACCACTGCTATCTTATGGAATCTTGGAGCTTGTGGAATCTGAGCAGTCCAGATGT 943  
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Qy 944 CTGCGGCGCATACCTGGGCGCTGATTGGGACTGCCATGACCCCAACTTCATCAGCAAGTTC 1003  
Db 611 CTACGAGCATACCTGGGCGCTGATTGGGACTGCCATGACCCCAACTTTTGTGAGCAATGTC 670  
Qy 1004 AACACTACTGTTGCTTTAAGCTGCACCTGCCGAGGCGAGCGCAACCTTACAGGACGAGTGT 1063  
Db 671 AACACCATGTTGCTTTAAGCTGCACCTGCCGAGGCGAGTGGCAACCTTGCAGGAGGAGTGT 730  
Qy 1064 GAAACGCTGGAAGGTCTTCTCCAGAAACCCCTGCTGCTGCGAGGCGCATTCAGCTAAG 1123  
Db 731 GAAATGCTGGAAGGTTCTTCTCCACAAACCCCTGCTGCTGCGAGGCGCATTCAGCTAAG 790  
Qy 1124 ATGCGTTTCCACAGACAGCTCTTCTCCAGAGCTGGGCGAGACTCTTACTTTTTCAGTGTGTG 1183  
Db 791 ATGCGTTTTCACGCCAACTCTTCTCCAGGACTGGGCCACACCCCTACTCTTGTCTGTGATG 850  
Qy 1184 CAGCAGCAGAACAGCAACCCCTGCTCTGAGACTGCAGCCCGAGGCTACCCATTTCTTTCTTTC 1243



Qy	1574	TCTGATGGTGATTAGCGGCTCACTCC-----AGCGTCTCTTCTGTTTCCCAGGAC	1625
Db	1485	TCTGGTGGTGACCAAGCTCCCAAGCCCTTTCTGAGCCCTTCTCTTGACTACCAAGAT	1544
Qy	1626	CACCCAGAGGCTAAGGAATCAGTCATTCCTCGTTGGCTTC-----TCCAGGAAG	1674
Db	1545	CA-CCAGAACTATTAAGTTAGCTTTCTCTATTGCANTCCAGATTAGGGTTAGGGTAGG	1603
Qy	1675	GCAGGCTAAGGGTTCTGAGGTGACTGAGAAAAATGTT-TCCTTTGTGTGGAAGGCTGGTG	1733
Db	1604	GAGSACTGGGTGTTCTGAGCGAGCTAGAAGTCATTTCTCTTTGTGGAAGAGGCTCCTG	1663
Qy	1734	CTCCAGGCTCCAGTCCCTCTGTAATGGAAGATAAAACCTGCTGGTGTCTTGACTGCTCT	1793
Db	1664	CCCCCTCGTCTCC--TCCTCTGATGGAGATGGAATACTACTGCCCTGCACCTGCCCTGTC	1721
Qy	1794	GCACGGCAATCTTGAACTTTGGGCATGAAGAGCTAAAGTCTTTGGGTCTTGTTTAACTC	1853
Db	1722	CCCGGATCTGCCGAACATCTGGGCATCAGAGCTGGAGGCTGTGGCCCTTGCTTTATTC	1781
Qy	1854	CTATTACTGTCGCCAAATCCCCTAGTCCCTTGGGTCAAGATTAACAATTT	1904
Db	1782	CTATTAATGTCCTAAAGTCTCTCTGGGCTCTTGATCATGATTAACACCTTT	1832

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RESULT 13
US-10-621-855-1
; Sequence 1, Application US/10621855
; Publication No. US20050221330A1
; GENERAL INFORMATION:
; APPLICANT: De Sauvage, Frederic J.
; APPLICANT: Klein, Richard D.
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Phillips, Heidi S.
; TITLE OF INVENTION: GFALPHA3 AND ITS USES
; FILE REFERENCE: GENENT.065A
; CURRENT APPLICATION NUMBER: US/10/621,855
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 09/272,835
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/079,124
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/081,569
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-621-855-1

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Qy	1626	CACCCAGAGGCTAAGCAATCAGTCATTTCCCTGTGTGCTTCTCCAGGAAGCGAGGCTAAGG	1685
Db	301	CACCCAGAGGCTAAGCAATCAGTCATTTCCCTGTGTGCTTCTCCAGGAAGCGAGGCTAAGG	360
Qy	1686	GTCTCTGAGGTGACTGAGAAAAATGTTT	1712
Db	361	GTCTCTGAGGTGACTGAGAAAAATGTTT	387

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RESULT 14
US-10-621-855-2
; Sequence 2, Application US/10621855
; Publication No. US20050221330A1
; GENERAL INFORMATION:
; APPLICANT: De Sauvage, Frederic J.
; APPLICANT: Klein, Richard D.
; APPLICANT: Rosenthal, Arnon
; APPLICANT: Phillips, Heidi S.
; TITLE OF INVENTION: GFRALPHA3 AND ITS USES
; FILE REFERENCE: GENENT.065A
; CURRENT APPLICATION NUMBER: US/10/621,855
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 09/272,835
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/079,124
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 60/081,569
; PRIOR FILING DATE: 1998-04-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 353
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-621-855-2

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RESULT 15  
US-10-305-720-530  
; Sequence 530, Application US/10305720  
; Publication No. US20040010136A1

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 22, 2006, 09:22:40 ; Search time 663 Seconds  
(without alignments)  
6805.204 Million cell updates/sec

Title: US-10-621-855-4  
Perfect score: 1935  
Sequence: 1 gaattggccctcgaggcca.....aaaaaaaaaaaaaaaaaa 1935

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues  
Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications NA\_New.\*
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  - 2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
  - 4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
  - 5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
  - 6: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
  - 7: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*
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  - 9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
  - 10: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
  - 11: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
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  - 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	544	28.1	600	12	US-11-136-527-4762
3	265	13.7	784	12	US-11-136-527-1671
4	227.6	11.8	600	12	US-11-136-527-5767
5	86	4.4	2787	12	US-11-136-527-3767
6	72.6	3.8	1707	8	US-10-955-054A-193
7	72.6	3.8	2542	8	US-10-955-054A-9
8	67.8	3.5	3673	12	US-11-136-527-246
9	44	2.3	574	6	US-09-925-065A-573503
10	44	2.3	574	6	US-09-925-065A-573504
11	40.8	2.1	629	12	US-11-136-527-1281
12	40.2	2.1	1400	12	US-11-136-527-7487
13	40.2	2.1	1494	12	US-11-136-527-3391
14	39.8	2.1	1494	8	US-10-444-926-9
15	39.4	2.0	522	6	US-09-925-065A-319364
16	39.4	2.0	522	6	US-09-925-065A-319365
17	39.4	2.0	2357	8	US-10-947-249-99
18	39.2	2.0	613	6	US-09-925-065A-556194
19	38.6	2.0	153376	12	US-11-121-086-5
20	38.6	2.0	172543	12	US-11-121-086-6

c	21	38.2	2.0	2341	8	US-10-821-234-199	Sequence 199, App
	22	38	2.0	3020	8	US-10-947-249-155	Sequence 155, App
	23	37.8	2.0	1280	12	US-11-000-463-214	Sequence 214, App
	24	37.6	1.9	537	6	US-09-925-065A-499837	Sequence 499837,
	25	37.6	1.9	560	6	US-09-925-065A-928692	Sequence 928692,
	26	37.6	1.9	560	6	US-09-925-065A-949884	Sequence 949884,
	27	37.6	1.9	562	6	US-09-925-065A-499835	Sequence 499835,
	28	37.6	1.9	562	6	US-09-925-065A-499836	Sequence 499836,
	29	37.6	1.9	1278	12	US-11-000-463-95	Sequence 95, Appl
	30	37.2	1.9	562	6	US-09-925-065A-499834	Sequence 499834,
	31	37.2	1.9	1400	12	US-11-136-527-4809	Sequence 4809, Ap
	32	37.2	1.9	2124	12	US-11-136-527-713	Sequence 713, App
c	33	37	1.9	482	6	US-09-925-065A-510953	Sequence 510953,
	34	37	1.9	535	6	US-09-925-065A-258873	Sequence 258873,
	35	37	1.9	567	6	US-09-925-065A-951524	Sequence 951524,
	36	37	1.9	579	6	US-09-925-065A-932296	Sequence 932296,
	37	37	1.9	579	6	US-09-925-065A-951523	Sequence 951523,
	38	37	1.9	585	6	US-09-925-065A-753184	Sequence 753184,
	39	37	1.9	647	12	US-11-000-463-230	Sequence 230, App
	40	37	1.9	1056	12	US-11-136-527-3921	Sequence 3921, Ap
c	41	36.8	1.9	587	6	US-09-925-065A-826467	Sequence 826467,
	42	36.8	1.9	604	6	US-09-925-065A-659494	Sequence 659494,
	43	36.8	1.9	612	6	US-09-925-065A-767121	Sequence 767121,
	44	36.8	1.9	621	6	US-09-925-065A-740743	Sequence 740743,
c	45	36.8	1.9	771	12	US-11-091-883-268	Sequence 268, App

ALIGNMENTS

RESULT 1

US-11-136-527-666  
; Sequence 666, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 666  
; LENGTH: 667  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-666

Query Match	31.2%	Score 604.6;	DB 12;	Length 667;
Best Local Similarity	94.2%	Pred. No. 1.7e-126;		
Matches 628;	Conservative 0;	Mismatches 39;	Indels 0;	Gaps 0;
QY	493	CACAGTGACCAAGCAACCCCTGGAATAATCTTTAGCAAGTTGAACATGCTCAAAACGAGA	552	
Db	1	CACAGTGACCAAGCAACCCCTGGAATAATCTTTAGCAAGTTGAACATGCTCAAAACGAGA	60	
QY	553	CTCGAGCTTGCCTCAAAATTTGCTGTGCTGTCTTCTTCCAGCAAGTGTGACCGCT	612	
Db	61	CTCGAGCTTGCCTCAAAATTTGCTGTGCTGTCTTCTTCCAGCAAGTGTGACCGCT	120	
QY	613	CGCAAGGCTTACGGGAGGATGCTCAGGATCCGCTGCCAGGCCACCTCTTGCTTACG	672	
Db	121	CGCAAGGCTTACGGGAGGATGCTCAGGATCCGCTGCCAGGCCACCTCTTGCTTACG	180	
QY	673	CCAGTGGCTCTCTTTTGAAGAGGACAGAGTCCACGCTCAGGCTGTGCTGTG	732	
Db	181	TCAGTGGCTCTCTTTTGAAGAGGACAGAGTCCACGCTCAGGCTGTGCTGTG	240	
QY	733	TCCCTGTGCACCAAGATGCGGCTGTGGGAGGGGGGCTGACACATGCCCCCAG	792	



Db 241 TCCCTGTGACCCGGAAGATGGGGCTGTGGGAGCGCGGCGAACACCATCGCCCCCAG 300  
Qy 793 TTGGCCCTGCTTCTGTAAACCCCAATTGCTGTGATCTGGGAGCTTCTGCGTGCGGA 852  
Db 301 TTGGCCCTGCGGTGTGGGCCCCCAACTGCTTAGATCTTCGGAGCTTCCGCGGTGGGA 360  
Qy 853 CCCTTTGTGCAGATCAGCCCTGATGGAATTCAGACCCCACTGTCTATCTATGGACATCCT 912  
Db 361 CCCTCTGTGCAGATCAGCCCTGATGGAATTCAGACCCCACTGTCTATCTATGGACATCCT 420  
Qy 913 TGGGACTGTGTCACTGAGCAGTCCAGATGTCTGGGGCATACTCTGGGGCTGATTTGGGAC 972  
Db 421 CGGGACTTGTGCACTGAGCAGTCCAGATGTCTGGGGCATACTCTGGGGCTGATTTGGGAC 480  
Qy 973 TGCCATGACCCCAAACTTTCATCAGCAAGGTCAACTACTGTGTGGCTTAAGCTGACCTG 1032  
Db 481 TGCCATGACCCCAAACTTTCATCAGCAAGGTCAACTACTGTGTGGCTTAAGCTGACCTG 540  
Qy 1033 CGAGGCGAGCGCAACCTTACAGGAGAGTGTGAACAGCTGGAAAGGTCTCTTCCAGAA 1092  
Db 541 CGAGGCGAGTGGCAACCTTTCAGGAGCAGTGTGAACAGCTGGAAAGGTCTCTTCCAGAA 600  
Qy 1093 CCCCTGCTGTGGAGGCCATTGACAGCTAAGATGCGTTTCCACAGACAGCTCTTCTCCCA 1152  
Db 601 CCCCTGCTGTGGAGGCCATTGCGGCTTAAATGCGTTTCCACAGACAACTCTTCTCCCA 660  
Qy 1153 GGACTGG 1159  
Db 661 GGACTGG 667

RESULT 2  
US-11-136-527-4762  
; Sequence 4762, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4762  
; LENGTH: 600  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-4762

Query Match 28.1%; Score 544; DB 12; Length 600;  
Best Local Similarity 94.2%; Pred. No. 7.3e-113;  
Matches 565; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
Qy 560 CTCCTGCTCAAAATTTGCTATGCTGTGTAATCTTTCAGCAAGTGTGACGCGCTGGCGAG 619  
Db 1 CTCCTGCTCAAAATTTGCTATGCTGTGTAATCTTTCAGCAAGTGTGACGCGCTGGCGAG 60  
Qy 620 GCCTACGGGGAGGATGCTCAGGGATCGCTGCGAGCGCACTCTGCTAGCCAGCTG 679  
Db 61 GCCTACGGGGAGGATGCTCAGGGATCGCTGCGAGCGCACTCTGCTAGCTAGCTG 120  
Qy 680 CGCTCCTCTTTTGAAGGACAGAGTCCACGCTCAGGGTCTGCTGTGTGCTCCCTGT 739  
Db 121 CGCTCCTCTTCTTGAAGGACAGAGTCCACGCTCAGGGCTGCTGTGTGCTCCCTGT 180  
Qy 740 GCACAGAAGATCGGGCTGTGGGAGCGGCGGCTTAACACCATCGCCCCCAGTTGGCC 799  
Db 181 GCACCGGAAGATCGGGCTGTGGGAGCGGCGGCTTAACACCATCGCCCCCAGTTGGCC 240  
Qy 800 CTGCTTCTGTAAACCCCAATTTGCTGTGATCTGCGGAGCTTCTGCGGTGCGGACCTTTG 859

Db 241 CTCCGCTGTGTGGCCCCCAACTGCTTAGATCTTCGGAGCTTCCGCGGTGGCGACCTCTG 300  
Qy 860 TGCGATCAGCCTGTGAGTGTCCAGACCCCACTGTCTATCTATGGACATCTTTGGGACT 919  
Db 301 TGCGATCAGCCTGTGAGTGTCCAGACCCCACTGTCTATCTATGGACATCTTCGGGACT 360  
Qy 920 TGTCAACTGAGCAGTCCAGATGTCTGGGGCATACTCTGGGGCTGATTTGGGACTGCCATG 979  
Db 361 TGTCAACTGAGCAGTCCAGATGTCTGGGGCATACTCTGGGGCTGATTTGGGACTGCCATG 420  
Qy 980 ACCCCAACTTTCATCAGCAAGGTCAACTACTGTGTGGCTTAAGCTGACCTGCGGAGGC 1039  
Db 421 ACCCCAACTTTCATCAGCAAGGTCAACTACTGTGTGGCTTAAGCTGACCTGCGGAGGC 480  
Qy 1040 AGCGGCAACCTTACAGGAGCAGTGTGAACAGCTGGAAAGGTCTCTTCCAGACCTTTC 1099  
Db 481 AGTGGCAACCTTTCAGGAGCAGTGTGAACAGCTGGAAAGGTCTCTTCCAGACCTTTC 540  
Qy 1100 CTGCTGGAGGCCATTGACAGCTAAGATGCGTTTCCACAGACAGCTCTTCTCCAGACTGG 1159  
Db 541 CTGCTGGAGGCCATTGCGGCTTAAATGCGTTTCCACAGACAACTCTTCTCCAGACTGG 600

RESULT 3  
US-11-136-527-1671/c  
; Sequence 1671, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1671  
; LENGTH: 784  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-1671

Query Match 13.7%; Score 265; DB 12; Length 784;  
Best Local Similarity 72.6%; Pred. No. 4.8e-50;  
Matches 451; Conservative 31; Mismatches 86; Indels 53; Gaps 10;  
Qy 1315 CCACACCCAGCACTGATTTGCGAGCCTGTGTGGGAGAGAACTCGCCAGCCTGTGGAAGAAG 1374  
Db 769 CTWCAYCCWAKCCGACTTGCAGCCTGTGATGGGAGAGAAATGCTGGCTCTGGAAGAAG 710  
Qy 1375 ACAGAGCTGTGTACACAGCAACCCGGAACCAACAGGCAATTCGCGAGACATCCCGCTG 1434  
Db 709 ATGCAACAGGCTCACT-----GCACATCTCTGCTG 679  
Qy 1435 CTCAGAGAGAGTCTT---AGAGTGGGGCTGTGACCCCTTC-CGATCCTGAGCGGCTAG 1490  
Db 678 CTCAGATGAGGTCTTGGMAGARGCGGGCTGTGACCGKCAKSRKSCGTGAGCGGCCAG 619  
Qy 1491 TTTTCAAACTTCCCTTGGCCCTGCTTCTTCTGGCTCAGGGCTGCTCTCTTTAGGACTTT 1550  
Db 618 CTTTCAAACTTCTGCTAC-----TWACTCTGCTGGGCTGCTCTCTCTAGGACCTT 566  
Qy 1551 GTGGGTCCAGTTTGGCTTCTGCTGATGTGATGAGGGGTACCTCCAGCGCTTCTT 1610  
Db 565 GT-ACCTCCAGTTTGGCTGTATATTGTGGTGTGATTAGCTTCCCACTCCAGCCCTTCTT 507  
Qy 1611 CTTGTTTCCAGGACCCAGAGCTAAGAAATCAGTCAATTCCTGTTGCTTCTCCAG 1670  
Db 506 CTTGTTTCCAGGACCCAG-CGCTAATGACTCACTCACTTCTCTGGTTCCTTCTCCAG 448